GenCore version 5.1.9

OM protein - protein search, using sw model

Run on: October 14, 2006, 07:52:47 ; Search time 201 Seconds
(without alignments)
427.645 Million cell updates/sec

Title: US-10-653-350-1
Perfect score: 960
Sequence: 1 MALTFALLVALLVLSCKSSC.....EIMRSFSLSTNLQESLRSKE 188

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	960	100.0	188	2	AAY42486	Aay42486 Human int
2	960	100.0	188	3	AAY69484	Aay69484 Amino aci
3	960	100.0	188	5	AAE15828	Aae15828 Human int
4	960	100.0	188	5	AAE18957	Aae18957 Human alp
5	960	100.0	188	5	ABB07434	Abb07434 Interfero
6	960	100.0	188	6	ABR55840	Abr55840 Human int
7	960	100.0	188	6	AAO16454	Aao16454 Human int
8	960	100.0	188	8	ADF77247	Adf77247 Interfero
9	960	100.0	188	8	ADL24486	Adl24486 Human int
10	960	100.0	188	8	ADN49676	Adn49676 Human int
11	960	100.0	188	8	ADU74352	Adu74352 Human int
12	960	100.0	188	9	ADZ46960	Adz46960 Human pre
13	960	100.0	188	9	AED67247	Aed67247 Wild-type
14	960	100.0	188	10	AEE63137	Aee63137 Human int
15	960	100.0	188	10	AEF69475	Aef69475 Human int
16	960	100.0	415	9	ADV97038	Adv97038 Human IFN
17	960	100.0	423	9	ADV97036	Adv97036 Human IFN
18	960	100.0	430	9	ADV97048	Adv97048 Human IFN
19	960	100.0	669	9	AED67013	Aed67013 pET32a-SD
20	960	100.0	773	7	ADF15107	Adf15107 Human alb
21	960	100.0	773	7	ADH21328	Adh21328 Human alb
22	960	100.0	773	9	ADW45446	Adw45446 Human int
23	960	100.0	773	9	AEB99999	Aeb99999 Albumin f
24	957	99.7	188	1	AAP20103	Aap20103 Sequence
25	957	99.7	188	4	AAB31458	Aab31458 Amino aci
26	957	99.7	188	5	AAE15826	Aae15826 Human int
27	957	99.7	188	5	ABB80767	Abb80767 Human int
28	957	99.7	188	8	ADJ99992	Adj99992 Human IFN
29	957	99.7	188	8	ADM41331	Adm41331 Human int
30	957	99.7	188	8	ADN02798	Adn02798 Human int
31	957	99.7	188	10	AEF69473	Aef69473 Human int
32	957	99.7	190	4	AAB82338	Aab82338 Human int
33	957	99.7	216	2	AAR38793	Aar38793 Natural h
34	957	99.7	431	8	ADW50827	Adw50827 Human int
35	957	99.7	432	8	ADW50823	Adw50823 Human int
36	957	99.7	433	8	ADW50825	Adw50825 Human int
37	954	99.4	188	8	ADF77281	Adf77281 Interfero
38	954	99.4	433	2	AAW18579	Aaw18579 Interfero
39	952	99.2	188	2	AAR20564	Aar20564 O-glycosy
40	952	99.2	188	2	AAR20549	Aar20549 Human IFN
41	951	99.1	418	9	ADV77270	Adv77270 IFN-alpha
42	944	98.3	187	1	AAP20007	Aap20007 Hybrid hu
43	941	98.0	184	9	ADZ51488	Adz51488 Truncated
44	937	97.6	183	9	ADZ51489	Adz51489 Truncated
45	937	97.6	219	2	AAR11356	Aar11356 Alkaline

ALIGNMENTS

RESULT 1
AAY42486
ID AAY42486 standard; protein; 188 AA.
XX
AC AAY42486;
XX
DT 15-FEB-2000 (first entry)
XX
DE Human interferon protein sequence.
XX
KW Wild type; human; interferon-alpha; plasmid; cytomegalovirus; CMV;
KW promoter; growth hormone; untranslated region; UTR; mammal; disease;
KW cancer.
XX
OS Homo sapiens.
XX
PN WO9947678-A2.
XX
PD 23-SEP-1999.
XX
PF 12-MAR-1999; 99WO-US005394.
XX
PR 19-MAR-1998; 98US-0078654P.
XX
PA (GENE-) GENEMEDICINE INC.
XX
PI Nordstrom J, Pericle F, Rolland A, Ralston R;
XX
DR WPI; 1999-562116/47.
DR N-PSDB; AAY40401.
XX
PT New plasmids containing an interferon-alpha coding sequence, used for the
PT treatment of a mammalian condition or disease, particularly cancer.
XX
PS Disclosure; Page 51-52; 137pp; English.
XX
CC This sequence represents the wild type human interferon-alpha amino acid
CC sequence. The invention relates to a novel plasmid comprising a
CC cytomegalovirus (CMV) promoter transcriptionally linked with an
CC interferon alpha (IFN-alpha) coding sequence, and a growth hormone 3'-
CC untranslated region (UTR). The plasmids can be used for treating a
CC mammalian condition or disease, particularly cancer
XX
SQ Sequence 188 AA;

Query Match 100.0%; Score 960; DB 2; Length 188;

```
  Best Local Similarity   100.0%;  Pred. No. 3.8e-90;
  Matches  188;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFG 60

Qy         61 FPQEEFGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FPQEEFGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEA 120

Qy        121 CVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNL 180

Qy        181 QESLRSKE 188
              ||||||||
Db        181 QESLRSKE 188


RESULT 2
AAY69484
ID   AAY69484 standard; protein; 188 AA.
XX
AC   AAY69484;
XX
DT   03-JUL-2000  (first entry)
XX
DE   Amino acid sequence of human interferon-alpha2B.
XX
KW   Human; interferon-alpha2B; IFN-MM gene; chicken magnum; transgenic avian;
KW   oviduct; viral particle; deleterious mutation; avian egg.
XX
OS   Synthetic.
OS   Homo sapiens.
OS   Gallus sp.
XX
PN   WO200011151-A2.
XX
PD   02-MAR-2000.
XX
PF   25-AUG-1999;   99WO-US019393.
XX
PR   25-AUG-1998;   98US-00139902.
XX
PA   (UYGE-) UNIV GEORGIA RES FOUND INC.
PA   (AVIG-) AVIGENICS INC.
XX
PI   Ivarie R,  Harvey AJ,  Murphy GF,  Rapp JC;
XX
DR   WPI; 2000-237645/20.
DR   N-PSDB; AAZ99577, AAZ99578.
XX
PT   Direct oviduct transgenesis of avians useful for expression of exogenous
PT   proteins in eggs and for assessing suitability of expression cassettes or
PT   to screen a preparation of viral particles for deleterious mutations.
XX
PS   Example 1; Page 53-54; 54pp; English.
XX
CC   The present sequence represents human interferon-alpha2B polypeptide. The
CC   polynucleotide was modified with codons for the chicken magnum, and used
CC   to construct a vector for use in the method of the invention. The
CC   specification describes a method for preparing a transgenic avian which
CC   expresses an exogenous protein substantially only in its oviduct. The
CC   method comprises delivering a nucleic acid expression cassette directly
CC   to the oviduct of an immature avian, where the nucleic acid expression
CC   cassette comprises a promoter active in the avian oviduct, and a nucleic
CC   acid sequence coding for an exogenous protein, linked to the promoter.
CC   The method can be used to screen a preparation of viral particles for
CC   deleterious mutations. It can also be used to test the suitability of a
CC   transgene for expression in an avian oviduct or for secretion of its
CC   expression product into the lumen of the oviduct and into eggs of an
CC   avian
XX
SQ   Sequence 188 AA;

  Query Match             100.0%;  Score 960;  DB 3;  Length 188;
  Best Local Similarity   100.0%;  Pred. No. 3.8e-90;
  Matches  188;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFG 60

Qy         61 FPQEEFGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FPQEEFGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEA 120

Qy        121 CVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNL 180

Qy        181 QESLRSKE 188
              ||||||||
Db        181 QESLRSKE 188


RESULT 3
AAE15828
ID   AAE15828 standard; protein; 188 AA.
XX
AC   AAE15828;
XX
DT   26-MAR-2002  (first entry)
XX
DE   Human interferon (IFN) alpha 2 protein.
XX
KW   Human; vaccine; immunostimulatory molecule; interferon; IFN; therapy;
KW   antigen presentation; vaccine; tumourigenesis; cancer; cytostatic;
KW   antitumour; antibacterial; virucide; fungicide; protozoacide.
XX
OS   Homo sapiens.
XX
PN   WO200188097-A1.
XX
PD   22-NOV-2001.
XX
PF   17-MAY-2001; 2001WO-AU000565.
XX
PR   17-MAY-2000; 2000AU-00007553.
XX
PA   (MONU ) UNIV MONASH.
XX
PI   Ralph SJ;
XX
DR   WPI; 2002-082990/11.
DR   N-PSDB; AAD25508.
XX
PT   New composition, useful for treatment and/or prophylaxis of cancer and
PT   tumor, comprises immunostimulatory molecule and animal cells cultured in
PT   presence of interferon to enhance antigen presenting function of the
PT   cells.
XX
PS   Claim 45; Page 96-97; 127pp; English.
XX
CC   The present invention relates to a composition of matter comprising an
CC   immunostimulatory molecule and animal cells cultured in the presence of
CC   at least one interferon (IFN) for a time and under conditions sufficient
CC   to enhance the antigen presenting function of the cells. The invention is
CC   used as vaccine. The composition is useful for treatment and/or
CC   prophylaxis of tumourigenesis, cancer, viral, bacterial, fungal and
CC   protozoal infections. The composition which comprises the soluble
CC   immunostimulatory molecule and the cultured animal cells is administered
CC   separately, sequentially or simultaneously to the patient. The present
CC   sequence is human IFN alpha 2 protein
XX
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SQ   Sequence 188 AA;

  Query Match             100.0%;  Score 960;  DB 5;  Length 188;
  Best Local Similarity   100.0%;  Pred. No. 3.8e-90;
  Matches  188;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFG 60

Qy         61 FPQEEFGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FPQEEFGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEA 120

Qy        121 CVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNL 180

Qy        181 QESLRSKE 188
              ||||||||
Db        181 QESLRSKE 188


RESULT 4
AAE18957
ID   AAE18957 standard; protein; 188 AA.
XX
AC   AAE18957;
XX
DT   21-MAY-2002  (first entry)
XX
DE   Human alpha-2b-interferon precursor protein.
XX
KW   Human; duckweed plant; alpha-2b-interferon; haemoglobin; vaccination;
KW   collagen; 450 oxidase; industrial; chemical process; therapeutic; enzyme.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .23
FT                   /label= Signal_peptide
FT   Protein         24. .188
FT                   /label= Mature_alpha_2b_interferon
XX
PN   WO200210414-A2.
XX
PD   07-FEB-2002.
XX
PF   26-JUL-2001; 2001WO-US023400.
XX
PR   31-JUL-2000; 2000US-0221705P.
PR   23-MAY-2001; 2001US-0293330P.
XX
PA   (BIOL-) BIOLEX INC.
XX
PI   Stomp A,  Dickey L,  Gasdaska J;
XX
DR   WPI; 2002-195966/25.
XX
PT   Producing recombinant polypeptides from duckweed plant culture, by
PT   transforming culture with nucleotide sequence coding for the polypeptide
PT   and signal peptide that directs polypeptide secretion into culture
PT   medium.
XX
PS   Claim 21; Page 45-46; 47pp; English.
XX
CC   The invention relates to a method for producing a biologically active
CC   recombinant polypeptide. The method comprises culturing a duckweed plant
CC   culture or duckweed nodule culture, which is stably transformed to
CC   express the polypeptide encoded by a nucleotide sequence that has been
CC   modified for enhanced expression in duckweed and collecting the
CC   polypeptide from duckweed plant or nodule culture. The method is useful
CC   for producing a biologically active recombinant polypeptide and for the
CC   directed secretion of the polypeptide from duckweed plant or nodule
CC   cultures. The polypeptides include a mammalian, therapeutic polypeptide
CC   such as insulin, interferons, monoclonal antibodies, cytokines, vaccines,
CC   in particular human alpha-2b-interferon or its biologically active
CC   variant. The duckweed frond culture or duckweed nodule culture expresses
CC   and assembles all of the subunits of a biologically active multimeric
CC   protein chosen from collagen, haemoglobin, P450 oxidase, and a monoclonal
CC   antibody, useful for industrial or chemical processes or for diagnostic,
CC   therapeutic or vaccination purposes. Nucleic acid encoding the
CC   recombinant polypeptides are useful for the expression and secretion of
CC   human alpha-2b-interferon in duckweed. The present sequence is human
CC   alpha-2b-interferon precursor protein
XX
SQ   Sequence 188 AA;

  Query Match             100.0%;  Score 960;  DB 5;  Length 188;
  Best Local Similarity   100.0%;  Pred. No. 3.8e-90;
  Matches  188;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFG 60

Qy         61 FPQEEFGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FPQEEFGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEA 120

Qy        121 CVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNL 180

Qy        181 QESLRSKE 188
              ||||||||
Db        181 QESLRSKE 188


RESULT 5
ABB07434
ID   ABB07434 standard; peptide; 188 AA.
XX
AC   ABB07434;
XX
DT   09-APR-2002  (first entry)
XX
DE   Interferon-alpha2 protein fragment.
XX
KW   Interferon-beta-2; IFN-beta2; neuroprotective; cytostatic; virucide;
KW   antiarthritic; antirheumatic; gene therapy; interferon-alpha2.
XX
OS   Unidentified.
XX
PN   WO200195929-A2.
XX
PD   20-DEC-2001.
XX
PF   18-JUN-2001; 2001WO-US041022.
XX
PR   16-JUN-2000; 2000US-0212046P.
PR   15-JUN-2001; 2001US-00881050.
XX
PA   (SCHD ) SCHERING AG.
XX
PI   Croze EM,  Faulds D,  Wagner TC;
XX
DR   WPI; 2002-130714/17.
XX
PT   Composition for treating multiple sclerosis, cancer and viral diseases
PT   and infections, comprises human interferon-beta-2 or its biologically-
PT   active fragment or derivative.
XX
PS   Disclosure; Fig 4; 61pp; English.
XX
CC   The invention relates to a pharmaceutical composition comprising a
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CC   therapeutically effective amount of human interferon-beta-2 (IFN-beta2)
CC   polypeptide. The composition is useful for treating multiple sclerosis in
CC   mammals, in particular a human in need of such treatment, and also cancer
CC   e.g. intraepithelial neoplasia and cervical cancer, autoimmune diseases
CC   e.g. rheumatoid arthritis and viral diseases or infections. The
CC   composition is useful for anti-oncogene regulation, antitumour activity,
CC   antiviral activity, cell growth inhibition or antigrowth activity, anti-
CC   proliferation, enhancement of cytotoxicity of lymphocytes, inducement or
CC   inhibition of differentiation of target cells, immunoregulatory activity,
CC   macrophage activation and down-regulation of oncogenes. Sequences
CC   ABB07427-441 represent various interferon (IFN) sequences used for
CC   alignment studies with the human IFN-beta2 polypeptide
XX
SQ   Sequence 188 AA;

  Query Match             100.0%;  Score 960;  DB 5;  Length 188;
  Best Local Similarity   100.0%;  Pred. No. 3.8e-90;
  Matches  188;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFG 60

Qy         61 FPQEEFGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FPQEEFGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEA 120

Qy        121 CVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNL 180

Qy        181 QESLRSKE 188
              ||||||||
Db        181 QESLRSKE 188


RESULT 6
ABR55840
ID   ABR55840 standard; protein; 188 AA.
XX
AC   ABR55840;
XX
DT   02-SEP-2003  (first entry)
XX
DE   Human interferon-alpha (IFN-alpha).
XX
KW   Peptide remodeling; glycoconjugation; glycosyltransferase; glycan;
KW   interferon-alpha; IFN-alpha; human.
XX
OS   Homo sapiens.
XX
PN   WO2003031464-A2.
XX
PD   17-APR-2003.
XX
PF   09-OCT-2002; 2002WO-US032263.
XX
PR   10-OCT-2001; 2001US-0328523P.
PR   19-OCT-2001; 2001US-0344692P.
PR   28-NOV-2001; 2001US-0334233P.
PR   28-NOV-2001; 2001US-0334301P.
PR   07-JUN-2002; 2002US-0387292P.
PR   25-JUN-2002; 2002US-0391777P.
PR   17-JUL-2002; 2002US-0396594P.
PR   16-AUG-2002; 2002US-0404249P.
PR   28-AUG-2002; 2002US-0407527P.
XX
PA   (NEOS-) NEOSE TECHNOLOGIES INC.
XX
PI   De Frees S,  Zopf D,  Bayer R,  Bowe C,  Hakes D,  Chen X;
XX
DR   WPI; 2003-449162/42.
DR   N-PSDB; ACC78870.
XX
PT   Remodeling a peptide, by removing a saccharyl subunit from the peptide to
PT   form truncated glycan, and adding or deleting glycosyl groups to a
PT   peptide and/or adding modifying group of a peptide to remodel the
PT   peptide.
XX
PS   Example; Fig 53B; 900pp; English.
XX
CC   The invention relates to a cell-free, in vitro method of remodeling a
CC   peptide. The method involves removing a saccharyl subunit from the
CC   peptide, thus forming a truncated glycan, and contacting the truncated
CC   glycan with at least one glycosyltransferase and at least one glycosyl
CC   donor under conditions suitable to transfer at least one glycosyl donor
CC   to the truncated glycan, thus remodeling the peptide. Conjugates can be
CC   formed between a granulocyte colony stimulating factor (G-CSF) peptide,
CC   interferon alpha peptide, interferon beta peptide, Factor VIIa peptide,
CC   Factor IX peptide, follicle stimulating hormone peptide, erythropoietin
CC   (EPO) peptide, granulocyte macrophage colony stimulating factor (GM-CSF)
CC   peptide, interferon-gamma peptide, alpha-1-protease inhibitor (A-1-PI)
CC   peptide, beta-glucosidase peptide, tissue plasminogen activator (TPA)
CC   peptide, interleukin-2 (IL-2) peptide, Factor VIII peptide, TNFalpha
CC   receptor/immunoglobulin (Ig) G fusion peptide, urokinase peptide, anti-
CC   glycoprotein IIb/IIIa monoclonal antibody peptide, chimeric anti HER2
CC   antibody peptide, anti-respiratory syncytial virus (RSV) F peptide, anti-
CC   CD20 antibody peptide, recombinant DNase peptide, anti-TNF alpha peptide,
CC   insulin peptide, hepatitis B surface antigen (HbsAg), human growth
CC   hormone (HGH) peptide, and a modifying group, where the modifying group
CC   is covalently attached to the peptide through an intact glycosyl linking
CC   group. The method is useful for a cell-free, in vitro method of
CC   remodeling the above mentioned peptides. The present sequence represents
CC   a human interferon-alpha (IFN-alpha)
XX
SQ   Sequence 188 AA;

  Query Match             100.0%;  Score 960;  DB 6;  Length 188;
  Best Local Similarity   100.0%;  Pred. No. 3.8e-90;
  Matches  188;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFG 60

Qy         61 FPQEEFGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FPQEEFGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEA 120

Qy        121 CVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNL 180

Qy        181 QESLRSKE 188
              ||||||||
Db        181 QESLRSKE 188


RESULT 7
AAO16454
ID   AAO16454 standard; protein; 188 AA.
XX
AC   AAO16454;
XX
DT   17-APR-2003  (first entry)
XX
DE   Human interferon alpha 2.
XX
KW   Human; cellular proliferation inhibitor; interferon alpha 2;
KW   single nucleotide polymorphism; SNP; cancer; tumour; metabolic disease;
KW   cardiovascular disease; infectious disease; immunological disease; HIV;
KW   central nervous system disease; wound healing; chemotherapy side effect;
KW   anaemia; osteoporosis; gastrointestinal disease; venereal disease; AIDS;
KW   obesity; hepatitis; infectious pneumonia; Alzheimer's disease; allergy;
KW   Parkinson's disease; multiple sclerosis; schizophrenia; depression;
KW   graft versus host disease; asthma; psoriasis; rheumatoid arthritis;
```

KW Crohn's disease; ulcerative colitis; genital wart.
XX
OS Homo sapiens.
XX
PN EP1236800-A2.
XX
PD 04-SEP-2002.
XX
PF 01-MAR-2002; 2002EP-00290515.
XX
PR 01-MAR-2001; 2001FR-00002843.
XX
PA (GENO-) GENODYSSEE.
XX
PI Escary J;
XX
DR WPI; 2003-185789/19.
DR N-PSDB; AAL51608.
XX
PT An isolated polynucleotide encoding interferon alpha 2 containing single
PT nucleotide polymorphisms is useful in treating disease.
XX
PS Claim 16; Page 33; 42pp; English.
XX
CC The invention comprises the amino acid and coding sequence of the human
CC interferon alpha 2 protein. The invention further relates to the
CC identification of single nucleotide polymorphisms (SNPs) within the human
CC interferon alpha 2 gene. The DNA and protein sequences of the invention
CC are useful for the treatment of: cancer; tumours; cardiovascular diseases
CC ; metabolic diseases; infectious diseases; central nervous system
CC diseases; immunological diseases; wound healing; chemotherapy side
CC effects; anaemia; osteoporosis; gastrointestinal diseases; venereal
CC diseases; obesity; hepatitis; HIV/AIDS; infectious pneumonias;
CC Alzheimer's disease; Parkinson's disease; multiple sclerosis;
CC schizophrenia; depression; graft versus host disease; allergies; asthma;
CC psoriasis; rheumatoid arthritis; Crohn's disease; ulcerative colitis; and
CC genital warts. The present amino acid sequence represents the human
CC interferon alpha 2 protein of the invention
XX
SQ Sequence 188 AA;

Query Match 100.0%; Score 960; DB 6; Length 188;
Best Local Similarity 100.0%; Pred. No. 3.8e-90;
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFG 60

Qy         61 FPQEEFGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FPQEEFGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEA 120

Qy        121 CVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNL 180

Qy        181 QESLRSKE 188
              ||||||||
Db        181 QESLRSKE 188
```

RESULT 8
ADF77247
ID ADF77247 standard; protein; 188 AA.
XX
AC ADF77247;
XX
DT 26-FEB-2004 (first entry)
XX
DE Interferon alpha.
XX
KW interferon alpha expression plasmid; tumour; IL-12.
XX
OS Unidentified.
XX
PN US2003181405-A1.
XX
PD 25-SEP-2003.
XX
PF 29-APR-2002; 2002US-00136837.
XX
PR 12-MAR-1999; 99US-00268135.
XX
PA (NORD/) NORDSTROM J L.
PA (PERI/) PERICLE F.
PA (ROLL/) ROLLAND A.
PA (RALS/) RALSTON R O.
XX
PI Nordstrom JL, Pericle F, Rolland A, Ralston RO;
XX
DR WPI; 2004-020834/02.
XX
PT A mammalian interferon alpha expression plasmid is useful in gene therapy
PT to deliver interferon alpha to cells to modulate tumor activity in the
PT treatment of cancer.
XX
PS Disclosure; SEQ ID NO 9; 65pp; English.
XX
CC The invention relates to a mammalian interferon alpha expression plasmid,
CC comprising a promoter and a synthetic 5' intron transcriptionally linked
CC with an interferon alpha coding sequence and a 3' untranslated region.
CC The mammalian interferon alpha expression plasmid is useful for treating
CC tumour growth. The present sequence is used in the exemplification of the
CC present invention.
XX
SQ Sequence 188 AA;

Query Match 100.0%; Score 960; DB 8; Length 188;
Best Local Similarity 100.0%; Pred. No. 3.8e-90;
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFG 60

Qy         61 FPQEEFGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FPQEEFGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEA 120

Qy        121 CVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNL 180

Qy        181 QESLRSKE 188
              ||||||||
Db        181 QESLRSKE 188
```

RESULT 9
ADL24486
ID ADL24486 standard; protein; 188 AA.
XX
AC ADL24486;
XX
DT 03-JUN-2004 (first entry)
XX
DE Human interferon alpha protein.
XX
KW human; interferon alpha isoform; glycosylation; antiinflammatory;
KW hepatotropic; virucide; neuroprotective; cytostatic; IFN alpha.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 31. .44

```
FT                   /note= "helix"
FT   Region          74. .90
FT                   /note= "helix"
FT   Region          139. .156
FT                   /note= "helix"
FT   Region          160. .180
FT                   /note= "helix"
XX
PN   WO2004019856-A2.
XX
PD   11-MAR-2004.
XX
PF   29-AUG-2003; 2003WO-KR001765.
XX
PR   31-AUG-2002; 2002KR-00052365.
XX
PA   (CJCJ-) CJ CORP.
XX
PI   Lee E,  Park H,  Kim H,  Park J,  Kim Y,  Lee H,  Koh H,  Oh M;
XX
DR   WPI; 2004-239105/22.
DR   N-PSDB; ADL24485.
XX
PT   New amino acid-modified human interferon alpha isoform having a sequence
PT   formed at a specific amino acid residue position where glycosylation is
PT   to take place, useful for treating e.g. chronic active hepatitis B.
XX
PS   Example 2; Fig 1; 52pp; English.
XX
CC   The present invention relates to a modified version of a human interferon
CC   alpha (IFN alpha) isoform having a sequence formed at a specific amino
CC   acid residue position so that glycosylation takes place at these sites.
CC   Interferon may be used for the treatment of chronic active hepatitis B,
CC   acute viral encephalitides, nasopharyngeal carcinoma, and the like. The
CC   present sequence is the human interferon alpha protein.
XX
SQ   Sequence 188 AA;

  Query Match             100.0%;  Score 960;  DB 8;  Length 188;
  Best Local Similarity   100.0%;  Pred. No. 3.8e-90;
  Matches  188;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFG 60

Qy         61 FPQEEFGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FPQEEFGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEA 120

Qy        121 CVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNL 180

Qy        181 QESLRSKE 188
              ||||||||
Db        181 QESLRSKE 188


RESULT 10
ADN49676
ID   ADN49676 standard; protein; 188 AA.
XX
AC   ADN49676;
XX
DT   15-JUL-2004  (first entry)
XX
DE   Human interferon alpha IFN-alpha protein SeqID 4.
XX
KW   human; erythropoietin; EPO; glycoconjugation; glycoPEGylated EPO peptide;
KW   anaemia; antianaemic; haematocrit level; kidney dialysis; haematology;
KW   interferon alpha; IFN-alpha.
XX
OS   Homo sapiens.
XX
PN   WO2004033651-A2.
XX
PD   22-APR-2004.
XX
PF   08-OCT-2003; 2003WO-US031974.
XX
PR   09-OCT-2002; 2002WO-US032263.
PR   05-NOV-2002; 2002US-00287994.
PR   06-JAN-2003; 2003US-00360770.
PR   19-FEB-2003; 2003US-00360779.
PR   09-APR-2003; 2003US-00410945.
XX
PA   (NEOS-) NEOSE TECHNOLOGIES INC.
XX
PI   De Frees S,  Zopf D,  Bayer R,  Bowe C,  Hakes D,  Chen X;
XX
DR   WPI; 2004-399848/37.
DR   N-PSDB; ADN49675.
XX
PT   Novel erythropoietin peptide comprising one or more glycans, having
PT   glycoconjugate molecule covalently attached to peptide, useful for
PT   treating anemia in mammal such as human.
XX
PS   Disclosure; SEQ ID NO 4; 1018pp; English.
XX
CC   This invention relates to novel erythropoietin (EPO) peptides and the
CC   remodelling and glycoconjugation of these naturally occurring peptides
CC   thereof. Specifically, each EPO peptide comprises one or more glycans and
CC   has a glycoconjugate molecule such as polyethylene glycol (PEG) attached
CC   to it. Accordingly, the present invention provides glycoPEGylated EPO
CC   peptides that have either monoantennary, biantennary or triantennary
CC   glycans covalently attached thereto. As such, these peptides are useful
CC   for the treatment of anaemia, and hence exhibit antianaemic activities
CC   working to increase haematocrit levels in mammals, in particular in
CC   humans i.e. increasing the relative volume of blood occupied by
CC   erythrocytes. Furthermore, EPO therapy can be used to treat kidney
CC   dialysis patients. This polypeptide is a human protein sequence related
CC   to the field of haematology, given in an exemplification of the
CC   invention.
XX
SQ   Sequence 188 AA;

  Query Match             100.0%;  Score 960;  DB 8;  Length 188;
  Best Local Similarity   100.0%;  Pred. No. 3.8e-90;
  Matches  188;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFG 60

Qy         61 FPQEEFGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FPQEEFGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEA 120

Qy        121 CVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNL 180

Qy        181 QESLRSKE 188
              ||||||||
Db        181 QESLRSKE 188


RESULT 11
ADU74352
ID   ADU74352 standard; protein; 188 AA.
XX
AC   ADU74352;
XX
DT   10-FEB-2005  (first entry)
XX
```

DE Human interferon-alpha.
XX
KW Hemostatic; Hepatotropic; Antianemic; Cytostatic; Osteopathic;
KW Antibacterial; Respiratory-Gen.; Antiinflammatory; Nephrotropic;
KW Antiinfertility; Antitubercular; Tuberculostatic; protein engineering;
KW bleeding; factor VIII deficiency; factor IX deficiency; liver cirrhosis;
KW infertility; anemia; end-stage renal disease; acute myelogenous leukemia;
KW osteoporosis; pulmonary fibrosis; tuberculosis.
XX
OS Homo sapiens.
XX
PN WO2004099231-A2.
XX
PD 18-NOV-2004.
XX
PF 09-APR-2004; 2004WO-US011494.
XX
PR 09-APR-2003; 2003US-00410897.
PR 09-APR-2003; 2003US-00410913.
PR 09-APR-2003; 2003US-00410930.
PR 09-APR-2003; 2003US-00410945.
PR 09-APR-2003; 2003US-00410962.
PR 09-APR-2003; 2003US-00410980.
PR 09-APR-2003; 2003US-00410997.
PR 09-APR-2003; 2003US-00411012.
PR 09-APR-2003; 2003US-00411026.
PR 09-APR-2003; 2003US-00411037.
PR 09-APR-2003; 2003US-00411043.
PR 09-APR-2003; 2003US-00411044.
PR 09-APR-2003; 2003US-00411049.
XX
PA (NEOS-) NEOSE TECHNOLOGIES INC.
XX
PI De Frees S, Zopf D, Bayer R, Bowe C, Hakes D, Chen X;
XX
DR WPI; 2004-833698/82.
DR N-PSDB; ADU74351.
XX
PT Cell-free in vitro method of remodeling peptide comprising poly(ethylene
PT glycol) useful for generating glycopeptide suitable for therapeutic uses
PT in mammal, involves addition or deletion of glycosyl groups to peptide.
XX
PS Disclosure; SEQ ID NO 4; 1024pp; English.
XX
CC The invention relates to a cell-free in vitro method (M1) of remodeling a
CC peptide comprising poly(ethylene glycol). (M1) is useful for remodeling
CC protein to generate glycopeptide having desired glycosylation pattern
CC suitable for therapeutic use in mammal. (M1) is useful for remodeling
CC peptides chosen from immunoglobulin, erythropoietin, tissue-type
CC activator peptide, etc. (M1) is useful for remodeling (a) G-CSF which is
CC useful for treating acute myeloid leukemia (AML), non-myeloid cancer
CC patient receiving bone marrow transplant, (b) factor VII for treating
CC bleeding episode, factor VIII deficiency, factor IX deficiency, liver
CC cirrhosis, (c) FSH for patients undergoing intrauterine insemination, in
CC vitro fertilization and for infertile patient, (d) EPO for treating
CC anemia, anemic patients having chronic renal insufficiency and end stage
CC renal disease, anemic patient undergoing dialysis, (e) GM-CSF for
CC treating acute myelogenous leukemia, (f) IFN-gamma for treating malignant
CC osteoporosis, pulmonary fibrosis, tuberculosis, cryptococcal meningitis,
CC etc. The glycopeptide produced using (M1) has specific customized or
CC desired glycosylation pattern. (M1) allows efficient production of
CC improved therapeutic moiety. The present sequence represents the amino
CC acid sequence of a protein remodelled in the present invention
XX
SQ Sequence 188 AA;

Query Match 100.0%; Score 960; DB 8; Length 188;
Best Local Similarity 100.0%; Pred. No. 3.8e-90;
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFG 60

Qy         61 FPQEEFGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FPQEEFGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEA 120

Qy        121 CVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNL 180

Qy        181 QESLRSKE 188
              ||||||||
Db        181 QESLRSKE 188
```

RESULT 12
ADZ46960
ID ADZ46960 standard; protein; 188 AA.
XX
AC ADZ46960;
XX
DT 30-JUN-2005 (first entry)
XX
DE Human precursor alpha 2B interferon.
XX
KW Protein production; interferon; transgenic plant; codon usage.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1. .24
FT /note= "Signal peptide"
FT Protein 24. .188
FT /note= "Mature interferon"
XX
PN WO2005035768-A1.
XX
PD 21-APR-2005.
XX
PF 16-APR-2004; 2004WO-US011968.
XX
PR 30-SEP-2003; 2003US-00675011.
PR 05-MAR-2004; 2004US-00794615.
XX
PA (BIOL-) BIOLEX INC.
XX
PI Dickey L, Gasdaska J, Cox K, Peele CG, Spencer D;
XX
DR WPI; 2005-306370/31.
XX
PT Producing a recombinant polypeptide in a duckweed plant or nodule culture
PT comprises culturing within a duckweed culture medium a duckweed plant
PT culture or a duckweed nodule culture, which is stably transformed to
PT express the polypeptide.
XX
PS Disclosure; SEQ ID NO 4; 62pp; English.
XX
CC The invention relates to producing human growth hormone, an antibody or
CC alpha-interferon in a duckweed plant culture or a duckweed nodule culture
CC comprising culturing within a duckweed culture medium a duckweed plant
CC culture or a duckweed nodule culture, where the duckweed plant or nodule
CC culture is stably transformed to express the polypeptide, and collecting
CC the polypeptide from the culture. Also included are producing human
CC growth hormone (M1) in a duckweed plant culture or a duckweed nodule
CC culture (comprising culturing within a duckweed culture medium a duckweed
CC plant culture or a duckweed nodule culture, where the duckweed plant or
CC nodule culture is stably transformed to express the human growth hormone,
CC and where human growth hormone is expressed from a nucleotide sequence
CC comprising a coding sequence for the human growth hormone and an operably
CC linked coding sequence for a signal peptide that directs secretion of the
CC human growth hormone into the culture medium and collecting the human
CC growth hormone from the duckweed culture medium), producing an antibody
CC (M2) in a duckweed plant culture or a duckweed nodule culture (comprising
CC the culturing and collecting steps in M1, and collecting the antibody

CC from the culture), producing human alpha-interferon (M3) in a duckweed
CC plant culture or a duckweed nodule culture (comprising culturing within a
CC duckweed culture medium a duckweed plant culture or a duckweed nodule
CC culture, where the duckweed plant or nodule culture is stably transformed
CC to express the human alpha;-interferon, and where the alpha-interferon is
CC expressed from a nucleotide sequence comprising the leader sequence from
CC the ribulose-bis-phosphate carboxylase small subunit 5B gene of Lemna
CC gibba operably linked to a coding sequence for the human growth hormone,
CC and an operably linked coding sequence for a signal peptide that directs
CC secretion of the alpha-interferon into the culture medium; and collecting
CC the alpha-interferon from the duckweed culture medium), the stably
CC transformed duckweed plant culture or duckweed nodule culture (I), human
CC growth hormone produced as in M1, an antibody produced according to M2,
CC alpha-interferon produced according to M3 and enhancing the expression
CC (M4) of a biologically active polypeptide in duckweed (comprising
CC culturing a duckweed plant or nodule culture, where the duckweed plant or
CC nodule culture is stably transformed to express the biologically active
CC polypeptide and where the biologically active polypeptide is expressed
CC from a nucleotide sequence comprising a coding sequence for the
CC biologically active polypeptide and an operably linked nucleotide
CC sequence comprising the leader from the ribulose-bis-phosphate
CC carboxylase small subunit gene of Lemna gibba). The method is useful for
CC producing human growth hormone in a duckweed plant culture or a duckweed
CC nodule culture. The methods are also useful for producing an antibody and
CC alpha-interferon in a duckweed plant culture. The method is useful for
CC enhancing the expression of a biologically active polypeptide in
CC duckweed. The present sequence represents human mature alpha 2B
CC interferon.
XX
SQ Sequence 188 AA;

```
  Query Match             100.0%;  Score 960;  DB 9;  Length 188;
  Best Local Similarity   100.0%;  Pred. No. 3.8e-90;
  Matches  188;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFG 60

Qy         61 FPQEEFGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FPQEEFGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEA 120

Qy        121 CVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNL 180

Qy        181 QESLRSKE 188
              ||||||||
Db        181 QESLRSKE 188
```

RESULT 13
AED67247
ID AED67247 standard; protein; 188 AA.
XX
AC AED67247;
XX
DT 12-JAN-2006 (first entry)
XX
DE Wild-type full length human interferon-alpha-2a polypeptide SEQ ID NO:23.
XX
KW interferon-alpha; endocrine-gen.; osteopathic; ophthalmological;
KW cytostatic; vasotropic; therapeutic.
XX
OS Homo sapiens.
XX
PN US2005220762-A1.
XX
PD 06-OCT-2005.
XX
PF 28-JAN-2005; 2005US-00046440.
XX
PR 02-FEB-2004; 2004US-0541528P.
PR 18-JUN-2004; 2004US-0580885P.
PR 18-JUN-2004; 2004US-0581175P.
PR 18-JUN-2004; 2004US-0581314P.
PR 22-DEC-2004; 2004US-0638616P.
XX
PA (AMBR-) AMBRX INC.
XX
PI Cho HS, Daniel TO, Hays A, Wilson TE;
XX
DR WPI; 2005-777263/79.
DR N-PSDB; AED67250.
XX
PT New human interferon polypeptide, useful for treating a disease, e.g.
PT gigantism, acromegaly, vascular eye disease, macular degeneration, or
PT sarcomas.
XX
PS Example 11; SEQ ID NO 23; 129pp; English.
XX
CC The invention relates to a novel human interferon (hIFN) polypeptide
CC comprising one or more non-naturally encoded amino acids. A hIFN
CC polypeptide of the invention has endocrine-gen., osteopathic,
CC ophthalmological, cytostatic, and vasotropic activity. The hIFN comprises
CC a sequence of 165 amino acids (AED67248) encoded by a nucleic acid
CC comprising a nucleotide sequence of 567 or 498 bp (AED67250 or AED67251).
CC The polypeptide, nucleic acid, composition, and method are useful for
CC treating a disease, e.g. gigantism, acromegaly, vascular eye disease,
CC macular degeneration, or sarcomas. The present sequence represents the
CC full length wild-type human interferon-alpha-2a polypeptide of the
CC invention.
XX
SQ Sequence 188 AA;

```
  Query Match             100.0%;  Score 960;  DB 9;  Length 188;
  Best Local Similarity   100.0%;  Pred. No. 3.8e-90;
  Matches  188;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFG 60

Qy         61 FPQEEFGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FPQEEFGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEA 120

Qy        121 CVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNL 180

Qy        181 QESLRSKE 188
              ||||||||
Db        181 QESLRSKE 188
```

RESULT 14
AEE63137
ID AEE63137 standard; protein; 188 AA.
XX
AC AEE63137;
XX
DT 09-FEB-2006 (first entry)
XX
DE Human interferon-alpha-2 amino acid sequence SEQ ID NO:8.
XX
KW myocardial disease; cardiovascular-gen.; interferon-alpha.
XX
OS Homo sapiens.
XX
PN US2005276785-A1.
XX
PD 15-DEC-2005.
XX
PF 07-JUN-2005; 2005US-00147492.

XX
PR 09-JUN-2004; 2004US-0579024P.
XX
PA (SCHD) SCHERING AG.
XX
PI Groetzbach G, Kapp J, Kuehl U, Schultheiss H, Sowade O;
PI Stuerzebecher C;
XX
DR WPI; 2006-028347/03.
DR N-PSDB; AEE63136.
XX
PT Composition, useful to treat e.g. cardiomyopathy, endothelial
PT dysfunction, arrhythmia, dyspnea and palpitations, comprises an isolated
PT interferon beta/interferon alpha or interferon beta/interferon alpha
PT mutein.
XX
PS Disclosure; SEQ ID NO 8; 69pp; English.
XX
CC The invention relates to a composition (A) having interferon-beta (IFN-
CC beta) or interferon-alpha (INF-alpha) activity. (A) comprises a
CC therapeutically affective amount of an isolated IFN-beta, IFN-alpha, IFN-
CC beta mutein or IFN-alpha mutein for treatment of cardiomyopathy and
CC endothelial dysfunction, where the therapeutically effective amount is in
CC a range from about 30 to 500 mcg. (A) is useful in the treatment of
CC cardiomyopathy and endothelial dysfunction, such as chronic inflammatory
CC cardiomyopathy, chronic viral cardiomyopathy, valvular cardiomyopathy,
CC ischemic cardiomyopathy, and hypertensive cardiomyopathy. The present
CC sequence represents human interferon-alpha-2 (IFN-alpha-2), which is
CC given in the exemplification of the present invention.
XX
SQ Sequence 188 AA;

Query Match 100.0%; Score 960; DB 10; Length 188;
Best Local Similarity 100.0%; Pred. No. 3.8e-90;
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFG 60
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Db          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFG 60

Qy         61 FPQEEFGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FPQEEFGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEA 120

Qy        121 CVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNL 180

Qy        181 QESLRSKE 188
              ||||||||
Db        181 QESLRSKE 188
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RESULT 15
AEF69475
ID AEF69475 standard; protein; 188 AA.
XX
AC AEF69475;
XX
DT 06-APR-2006 (first entry)
XX
DE Human interferon-alpha 2b.
XX
KW transgenic plant; interferon-alpha 2b; Antiinflammatory; Hepatotropic;
KW Virucide; cytostatic; Anti-HIV; Immunomodulator; hepatitis; cancer;
KW protein engineering; immune modulation.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1. .23
FT /label= signal_peptide
FT Protein 24. .188
FT /label= Mature_interferon-alpha_2b
XX
PN US2006024272-A1.
XX
PD 02-FEB-2006.
XX
PF 29-JUN-2005; 2005US-00172549.
XX
PR 29-JUL-2004; 2004US-0592479P.
XX
PA (LARG-) LARGE SCALE BIOLOGY CORP.
XX
PI Reinl SJ, Pogue GP;
XX
DR WPI; 2006-135331/14.
DR N-PSDB; AEF69474.
XX
PT Novel C-terminally truncated interferon polypeptide having enhanced
PT biological activity, useful for treating interferon affected disorder
PT such as viral hepatitis, hairy cell leukemia, Kaposi's sarcoma and immune
PT disorders.
XX
PS Example 1; SEQ ID NO 23; 54pp; English.
XX
CC The present sequence of human interferon-alpha 2b, related to the novel
CC polypeptides of the current invention comprising human C-terminally
CC truncated interferon (IFN) having enhanced biological activity, is
CC encoded by a nucleotide insert AEF69474, cloned into the viral vector
CC DN15. Type I interferons exhibit a wide range of biological activity,
CC including antiviral, anti-proliferative, neoplastic and immunomodulatory
CC activities. Interferon-alpha is produced by human leukocytes. Plant-
CC produced IFN-alpha, fused to an extensin signal peptide and an
CC endoplasmic reticulum retention signal, demonstrates anti-viral and anti-
CC proliferative activities comparable to the bacterially produced protein
CC but contains C-terminal truncations that predominantly occur during the
CC processing of the plant material. The plant is Nicotiana benthamiana. To
CC assemble human interferon-alpha 2b for expression in tobacco mosaic virus
CC (TMV), an assembly reaction containing each of 16 oligonucleotides,
CC AEF69455, AEF69456, AEF69457, AEF69458, AEF69459, AEF69460, AEF69461,
CC AEF69462, AEF69463, AEF69464, AEF69465, AEF69466, AEF69467, AEF69468,
CC AEF69469, and AEF69470, were added to a PCR reaction. The amplification
CC product was re-amplified using the oligonucleotides AEF69455, and
CC AEF69470. IFN-alpha 2a was amplified under the same conditions except
CC that the oligonucleotide, AEF69457, was replaced by AEF69471. The
CC amplified sequences were blunt-cloned into TOPO TA cloning vector and
CC clones with the correct sequence were cloned into viral vector DN15.
CC Infectious transcripts were synthesized in vitro and used to inoculate 23
CC day post sow N. benthamiana plants. Systemically infected tissue was
CC harvested at 10 days post inoculation and protein extracted by either
CC homogenization or vacuum infiltration. C-terminally truncated interferon
CC is useful for treating an interferon affected disorder, which involves
CC administering the composition of the invention to a patient, where the
CC interferon affected disorders are viral hepatitis, cancer such as hairy
CC cell leukemia, Kaposi's sarcoma, chronic myelogenous leukemia and
CC metastatic malignant melanoma, and immune disorders. C-terminally
CC truncated interferon has enhanced biological activity such as anti-
CC proliferative activity and improved processing qualities such as
CC stability in crude extracts, yield and homogeneity at the C-terminus. C-
CC terminally truncated interferon can be purified easily, and has enhanced
CC anti-viral and immune modulatory activities.
XX
SQ Sequence 188 AA;

Query Match 100.0%; Score 960; DB 10; Length 188;
Best Local Similarity 100.0%; Pred. No. 3.8e-90;
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFG 60

Qy         61 FPQEEFGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db         61 FPQEEFGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEA 120

Qy        121 CVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNL 180

Qy        181 QESLRSKE 188
              ||||||||
Db        181 QESLRSKE 188
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Search completed: October 14, 2006, 07:56:45
Job time : 205 secs

GenCore version 5.1.9

OM protein - protein search, using sw model

Run on: October 14, 2006, 07:57:02 ; Search time 41 Seconds
(without alignments)
441.189 Million cell updates/sec

Title: US-10-653-350-1
Perfect score: 960
Sequence: 1 MALTFALLVALLVLSCKSSC.....EIMRSFSLSTNLQESLRSKE 188

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	957	99.7	188	1	IVHUA2	interferon alpha-2
2	851	88.6	165	2	I78570	alpha 2 interferon
3	809.5	84.3	189	1	IVHUA7	interferon alpha-5
4	808.5	84.2	189	1	IVHUI6	interferon alpha-I
5	793.5	82.7	189	1	IVHU14	interferon alpha-I
6	781.5	81.4	189	2	I52347	interferon alpha-M
7	779.5	81.2	189	2	I51970	interferon precurs
8	772.5	80.5	189	1	IVHUA1	interferon alpha-1
9	770.5	80.3	189	1	IVHU4B	interferon alpha-I
10	768.5	80.1	189	2	I84464	interferon-alpha-F
11	767.5	79.9	189	1	IVHU16	interferon alpha-I
12	766.5	79.8	189	1	IVHUA5	interferon alpha-5
13	766.5	79.8	189	1	IVHUF	interferon alpha-I
14	760.5	79.2	189	1	IVHUA9	interferon alpha-1
15	756.5	78.8	189	2	I37584	IFN-alpha-N-protei
16	754.5	78.6	189	1	IVHUI8	interferon alpha-I
17	748.5	78.0	189	2	I53102	interferon-alpha-J
18	744.5	77.6	189	1	IVHUA0	interferon alpha-7
19	739.5	77.0	181	2	I56313	interferon alpha 2
20	732.5	76.3	189	1	IVHUA4	interferon alpha-4
21	728.5	75.9	176	2	I56314	interferon-alpha -
22	722.5	75.3	184	1	IVHOA4	interferon alpha-I
23	719.5	74.9	167	2	D25843	interferon alpha-G
24	718.5	74.8	184	1	IVHOA2	interferon alpha-I
25	710.5	74.0	184	1	IVHOA3	interferon alpha-I
26	704.5	73.4	184	1	IVHOA1	interferon alpha-I
27	690.5	71.9	167	2	E25843	interferon alpha-F
28	678.5	70.7	167	2	F25843	interferon alpha-J
29	665.5	69.3	162	2	C25843	interferon alpha-B
30	640.5	66.7	189	2	S23709	interferon alpha-1
31	603.5	62.9	189	1	IVMSA5	interferon alpha-I
32	596.5	62.1	189	1	IVBOI1	interferon alpha-I
33	591.5	61.6	189	1	IVBOID	interferon alpha-I
34	590.5	61.5	189	1	IVBOIA	interferon alpha-I
35	590.5	61.5	189	1	IVBOIB	interferon alpha-I
36	588.5	61.3	189	1	IVMSA1	interferon alpha-I
37	581.5	60.6	189	1	IVBOIC	interferon alpha-I
38	580.5	60.5	190	2	I49774	alpha-interferon -
39	579.5	60.4	190	2	A24401	interferon alpha-I
40	572.5	59.6	190	1	IVMSA2	interferon alpha-2
41	568.5	59.2	192	1	IVRTA1	interferon alpha-I
42	561.5	58.5	190	2	I49772	interferon alpha-7
43	561.5	58.5	190	2	I49775	interferon alpha-B
44	554.5	57.8	189	1	IVMSA6	interferon alpha-I
45	552.5	57.6	189	2	I49773	murine interferon

ALIGNMENTS

RESULT 1
IVHUA2
interferon alpha-2 precursor (allele a) [validated] - human
N;Alternate names: IFN-alpha2; interferon alpha-3; interferon alpha-A; leukocyte interfe
C;Species: Homo sapiens (man)
C;Date: 31-Oct-1980 #sequence_revision 01-Sep-1981 #text_change 09-Jul-2004
C;Accession: A93234; D93249; A93888; I59458; A94252; A25843; A01828; C61478; S15848; B4
R;Goeddel, D.V.; Yelverton, E.; Ullrich, A.; Heyneker, H.L.; Miozzari, G.; Holmes, W.;
ss, M.; Familletti, P.C.; Pestka, S.
Nature 287, 411-416, 1980
A;Title: Human leukocyte interferon produced by Escherichia coli is biologically active.
A;Reference number: A93234; MUID:81052322; PMID:6159538
A;Accession: A93234
A;Molecule type: DNA
A;Residues: 1-188 <GOE>
A;Cross-references: UNIPROT:P01563; UNIPARC:UPI000012D643; GB:V00544; NID:g32730; PIDN:(
A;Experimental source: clone pL31
R;Goeddel, D.V.; Leung, D.W.; Dull, T.J.; Gross, M.; Lawn, R.M.; McCandliss, R.; Seeburg
Nature 290, 20-26, 1981
A;Title: The structure of eight distinct cloned human leukocyte interferon cDNAs.
A;Reference number: A93249; MUID:81148795; PMID:6163083
A;Accession: D93249
A;Molecule type: mRNA
A;Residues: 1-188 <GO2>
A;Cross-references: UNIPARC:UPI000012D643; GB:V00549; NID:g32744; PIDN:CAA23810.1; PID:g
A;Note: eight classes of interferon alpha clones were identified; this sequence is deriv
R;Lawn, R.M.; Gross, M.; Houck, C.M.; Franke, A.E.; Gray, P.V.; Goeddel, D.V.
Proc. Natl. Acad. Sci. U.S.A. 78, 5435-5439, 1981
A;Title: DNA sequence of a major human leukocyte interferon gene.
A;Reference number: A93888; MUID:82060261; PMID:6170983
A;Accession: A93888
A;Molecule type: DNA
A;Residues: 1-45,'R',47-188 <LAW>
A;Cross-references: UNIPARC:UPI0000034B3A; GB:J00207; NID:g184581; PIDN:AAB59402.1; PID:
A;Experimental source: clone lambda-alpha-2
R;Oliver, G.; Balbas, P.; Valle, F.; Soberon, X.; Bolivar, F.
Rev. Latinoam. Microbiol. 27, 141-150, 1985
A;Title: [Cloning of human leukocyte interferon cDNA and a strategy for its production i
A;Reference number: I59458; MUID:86069501; PMID:3906813
A;Accession: I59458
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-188 <RES>
A;Cross-references: UNIPARC:UPI000012D643; GB:M54886; NID:g186498; PIDN:AAA59181.1; PID:
R;Streuli, M.; Nagata, S.; Weissmann, C.
Science 209, 1343-1347, 1980
A;Title: At least three human type alpha interferons: structure of alpha2.
A;Reference number: A94252; MUID:81015442; PMID:6158094
A;Accession: A94252
A;Molecule type: mRNA
A;Residues: 7-45,'R',47-188 <STR>
A;Cross-references: UNIPARC:UPI000002C6D4; GB:V00548; NID:g32740; PIDN:CAA23809.1; PID:g

R;Ohara, O.; Teraoka, H.
FEBS Lett. 211, 78-82, 1987
A;Title: Anomalous behavior of human leukocyte interferon subtypes on polyacrylamide gel
A;Reference number: A91374; MUID:87105954; PMID:3803589
A;Accession: A25843
A;Status: nucleic acid sequence not shown; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 'M',24-188 <OHA>
A;Cross-references: UNIPARC:UPI000002C5A3
A;Note: engineered sequence of mature form expressed in Eschericia coli
R;Allen, G.; Fantes, K.H.
Nature 287, 408-411, 1980
A;Title: A family of structural genes for human lymphoblastoid (leukocyte-type) interfer
A;Reference number: A01828; MUID:81052321; PMID:6159537
A;Accession: A01828
A;Molecule type: protein
A;Residues: 24-42,'Z',44-45,'R',47-74,'A',76,'S',78-98,'X',100-105,'D',107-109,'P',111-1
A;Cross-references: UNIPARC:UPI000017365A; UNIPARC:UPI000017365B
A;Note: residues at positions 83, 86, and 139 may be Ile or possibly Leu; those at posit
A;Note: 57-Arg, 75-Thr, 77-Pro, and 96-Glx were also found
R;Fukuda, S.; Ando, S.; Sanou, O.; Taniai, M.; Fujii, M.; Masaki, N.; Nakamura, K.I.; An
Lymphokine Res. 7, 175-185, 1988
A;Title: Simultaneous production of natural human tumor necrosis factor-alpha, -beta and
A;Reference number: A61478; MUID:88301617; PMID:2841543
A;Accession: C61478
A;Molecule type: protein
A;Residues: 24-45,'R',47-53 <FUK>
A;Cross-references: UNIPARC:UPI000017365C
A;Experimental source: B-cel lymphoblastoid cel line BALL-1
R;Adolf, G.R.; Kalsner, I.; Ahorn, H.; Maurer-Fogy, I.; Cantell, K.
Biochem. J. 276, 511-518, 1991
A;Title: Natural human interferon-alpha-2 is O-glycosylated.
A;Reference number: S15848; MUID:91264809; PMID:2049076
A;Accession: S15848
A;Molecule type: protein
A;Residues: 24-45,'R',47-53 <BIO>
A;Cross-references: UNIPARC:UPI000017365C
A;Experimental source: leukocytes
R;Zoon, K.C.; Miller, D.; Bekisz, J.; zur Nedden, D.; Enterline, J.C.; Nguyen, N.Y.; Hu,
J. Biol. Chem. 267, 15210-15216, 1992
A;Title: Purification and characterization of multiple components of human lymphoblastoi
A;Reference number: A42753; MUID:92340576; PMID:1634550
A;Accession: B42753
A;Molecule type: protein
A;Residues: 'X',25-45,'R',47-51,'X',53-55,'XX',58-65 <ZOO>
A;Cross-references: UNIPARC:UPI000017365D
A;Experimental source: Sendai virus-induced Namalwa cells
R;Wetzel, R.
Nature 289, 606-607, 1981
A;Title: Assignment of the disulphide bonds of leukocyte interferon.
A;Reference number: A93244; MUID:81123083; PMID:6162107
A;Contents: annotation; disulfide bonds
R;Murgolo, N.J.; Windsor, W.T.; Hruza, A.; Reichert, P.; Tsarbopoulos, A.; Baldwin, S.;
Proteins 17, 62-74, 1993
A;Title: A homology model of human interferon alpha-2.
A;Reference number: A44748; MUID:94052087; PMID:8234245
A;Contents: annotation; theoretical model
R;Gewert, D.; Salom, C.; Barber, K.; Macbride, S.; Cooper, H.; Lewis, A.; Wood, J.; Crow
J. Interferon Res. 13, 227-231, 1993
A;Title: Analysis of interferon-alpha 2 sequences in human genomic DNA.
A;Reference number: I56312; MUID:93375201; PMID:8366289
A;Accession: I56312
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-72 <REW>
A;Cross-references: UNIPARC:UPI00000701A9; GB:S64979; NID:g408874; PIDN:AAD13960.1; PID:
R;Zhao, X.X.; Li, B.L.; Langer, J.A.; Van Riper, G.; Pestka, S.
Anal. Biochem. 178, 342-347, 1989
A;Title: Construction and phosphorylation of a fusion protein Hu-IFN-alpha A/gamma.
A;Reference number: I36908; MUID:89321045; PMID:2502045
A;Accession: I36909
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 'M',24-188 <RE2>
A;Cross-references: UNIPARC:UPI000002C5A3; EMBL:X15631; NID:g22771; PIDN:CAA33638.1; PI
C;Genetics:
A;Gene: GDB:IFNA2
A;Cross-references: GDB:136359; OMIM:147562
A;Map position: 9p22-9p22
C;Superfamily: interferon alpha
C;Keywords: antiviral; cytokine; glycoprotein; leukocyte
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-188/Product: interferon alpha-2 #status experimental <MAT>
F;24-121,52-161/Disulfide bonds: #status experimental
F;129/Binding site: carbohydrate (Thr) (covalent) #status experimental

Query Match 99.7%; Score 957; DB 1; Length 188;
Best Local Similarity 99.5%; Pred. No. 3.5e-81;
Matches 187; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFG 60
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Db          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRKISLFSCLKDRHDFG 60

Qy         61 FPQEEFGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FPQEEFGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEA 120

Qy        121 CVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNL 180

Qy        181 QESLRSKE 188
              ||||||||
Db        181 QESLRSKE 188
```

RESULT 2
I78570
alpha 2 interferon - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
C;Accession: I78570
R;Weber, H.; Weissmann, C.
Nucleic Acids Res. 11, 5661-5669, 1983
A;Title: Formation of genes coding for hybrid proteins by recombination between related
A;Reference number: I58213; MUID:83299241; PMID:6310510
A;Accession: I78570
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-165 <RES>
A;Cross-references: UNIPROT:P01563; UNIPARC:UPI0000049830; GB:M29883; NID:g184585; PIDN
C;Genetics:
A;Gene: IFNA
C;Superfamily: interferon alpha

Query Match 88.6%; Score 851; DB 2; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.9e-71;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         24 CDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFGFPQEEFGNQFQKAETIPVLHEMI 83
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFGFPQEEFGNQFQKAETIPVLHEMI 60

Qy         84 QQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEACVIQGVGVTETPLMKEDSILAVR 143
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 QQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEACVIQGVGVTETPLMKEDSILAVR 120

Qy        144 KYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNLQESLRSKE 188
              |||||||||||||||||||||||||||||||||||||||||||||
Db        121 KYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNLQESLRSKE 165
```

RESULT 3
IVHUA7
interferon alpha-5 precursor - human

```
N;Alternate names: interferon alpha-G
C;Species: Homo sapiens (man)
C;Date: 01-Sep-1981 #sequence_revision 29-Jan-1999 #text_change 09-Jul-2004
C;Accession: S43716; A01833
R;Henco, K.; Brosius, J.; Fujisawa, A.; Fujisawa, J.I.; Haynes, J.R.; Hochstadt, J.; Kov
J. Mol. Biol. 185, 227-260, 1985
A;Title: Structural relationship of human interferon alpha genes and pseudogenes.
A;Reference number: A92916; MUID:86037205; PMID:4057246
A;Accession: S43716
A;Molecule type: DNA
A;Residues: 1-189 <HEN>
A;Cross-references: UNIPROT:P01569; UNIPARC:UPI0000047760; EMBL:X02956; NID:g32659; PIDN
R;Goeddel, D.V.; Leung, D.W.; Dull, T.J.; Gross, M.; Lawn, R.M.; McCandliss, R.; Seeburg
Nature 290, 20-26, 1981
A;Title: The structure of eight distinct cloned human leukocyte interferon cDNAs.
A;Reference number: A93249; MUID:81148795; PMID:6163083
A;Accession: A01833
A;Molecule type: mRNA
A;Residues: 57-189 <GOE>
A;Cross-references: UNIPARC:UPI0000141F4A; GB:V00541; GB:J00213; NID:g32718; PIDN:CAA238
A;Note: eight classes of interferon alpha clones were identified; this sequence is deriv
C;Genetics:
A;Gene: GDB:IFNA5
A;Cross-references: GDB:136362; OMIM:147565
A;Map position: 9p22-9p22
C;Superfamily: interferon alpha
C;Keywords: antiviral; cytokine; leukocyte
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-189/Product: interferon alpha-5 #status predicted <MAT>

  Query Match             84.3%;  Score 809.5;  DB 1;  Length 189;
  Best Local Similarity   83.6%;  Pred. No. 1.6e-67;
  Matches  158;  Conservative   11;  Mismatches   19;  Indels    1;  Gaps    1;

Qy          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFG 60
              ||| | ||:||:||:||| ||:|||||||||| :|||||::||| ||| ||||||||||
Db          1 MALPFVLLMALVVLNCKSICSLGCDLPQTHSLSNRRTLMIMAQMGRISPFSCLKDRHDFG 60

Qy         61 FPQEEF-GNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLE 119
              |||||| ||||||| | |||||||| |||||||||| ||||||||||||||||||||
Db         61 FPQEEFDGNQFQKAQAISVLHEMIQQTFNLFSTKDSSATWDETLLDKFYTELYQQLNDLE 120

Qy        120 ACVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTN 179
              ||::| ||| :|||| |||| |||||||||||| |||||||||||||||||||| |
Db        121 ACMMQEVGVEDTPLMNVDSILTVRKYFQRITLYLTEKKYSPCAWEVVRAEIMRSFSLSAN 180

Qy        180 LQESLRSKE 188
              ||| || ||
Db        181 LQERLRRKE 189


RESULT 4
IVHUI6
interferon alpha-I-6 precursor - human
N;Alternate names: HuIFN-alpha-I-6; LeIF K; type I interferon
C;Species: Homo sapiens (man)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 09-Jul-2004
C;Accession: A23753
R;Henco, K.; Brosius, J.; Fujisawa, A.; Fujisawa, J.I.; Haynes, J.R.; Hochstadt, J.; Kov
J. Mol. Biol. 185, 227-260, 1985
A;Title: Structural relationship of human interferon alpha genes and pseudogenes.
A;Reference number: A92916; MUID:86037205; PMID:4057246
A;Accession: A23753
A;Molecule type: DNA
A;Residues: 1-189 <HEN>
A;Cross-references: UNIPROT:P05013; UNIPARC:UPI000004775F; GB:X02958; NID:g32662; PIDN:C
C;Genetics:
A;Gene: GDB:IFNA6
A;Cross-references: GDB:136363; OMIM:147566
A;Map position: 9p22-9p22
C;Superfamily: interferon alpha
C;Keywords: antiviral
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-189/Product: interferon alpha-I-6 #status predicted <MAT>
F;24-122,52-162/Disulfide bonds: #status predicted

  Query Match             84.2%;  Score 808.5;  DB 1;  Length 189;
  Best Local Similarity   85.7%;  Pred. No. 1.9e-67;
  Matches  162;  Conservative    6;  Mismatches   20;  Indels    1;  Gaps    1;

Qy          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFG 60
              ||| |||| :|| :||||||||| |||||||||| |||:||||||||||||||||||||
Db          1 MALPFALLMALVVLSCKSSCSLDCDLPQTHSLGHRRTMMLLAQMRRISLFSCLKDRHDFR 60

Qy         61 FPQEEF-GNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLE 119
              |||||| |||||||| | ||||:||| |||||||||| |||| |||| ||||||||||||
Db         61 FPQEEFDGNQFQKAEAISVLHEVIQQTFNLFSTKDSSVAWDERLLDKLYTELYQQLNDLE 120

Qy        120 ACVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTN 179
              |||:| | |  |||| |||||||||||||||| |||||||||||||||||| | |
Db        121 ACVMQEVWVGGTPLMNEDSILAVRKYFQRITLYLTEKKYSPCAWEVVRAEIMRSFSSSRN 180

Qy        180 LQESLRSKE 188
              ||| || ||
Db        181 LQERLRRKE 189


RESULT 5
IVHU14
interferon alpha-I-14 precursor [validated] - human
N;Alternate names: HuIFN-alpha-I-14; lambda-2-h; type I interferon
C;Species: Homo sapiens (man)
C;Date: 01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change 09-Jul-2004
C;Accession: A92916; A94255; B93249; PC2203; A01834; C23753
R;Henco, K.; Brosius, J.; Fujisawa, A.; Fujisawa, J.I.; Haynes, J.R.; Hochstadt, J.; Kov
J. Mol. Biol. 185, 227-260, 1985
A;Title: Structural relationship of human interferon alpha genes and pseudogenes.
A;Reference number: A92916; MUID:86037205; PMID:4057246
A;Accession: A92916
A;Molecule type: DNA
A;Residues: 1-189 <HEN>
A;Cross-references: UNIPROT:P01570; UNIPARC:UPI00000541D5; GB:X02959; NID:g32650; PIDN:C
R;Lawn, R.M.; Adelman, J.; Dull, T.J.; Gross, M.; Goeddel, D.; Ullrich, A.
Science 212, 1159-1162, 1981
A;Title: DNA sequence of two closely linked human leukocyte interferon genes.
A;Reference number: A94255; MUID:81201124; PMID:6165082
A;Accession: A94255
A;Molecule type: DNA
A;Residues: 1-189 <LAW>
A;Cross-references: UNIPARC:UPI00000541D5; GB:V00533; GB:J00215; NID:g32635; PIDN:CAA237
R;Goeddel, D.V.; Leung, D.W.; Dull, T.J.; Gross, M.; Lawn, R.M.; McCandliss, R.; Seeburg
Nature 290, 20-26, 1981
A;Title: The structure of eight distinct cloned human leukocyte interferon cDNAs.
A;Reference number: A93249; MUID:81148795; PMID:6163083
A;Accession: B93249
A;Molecule type: mRNA
A;Residues: 1-174,'F',176-189 <GOE>
A;Cross-references: UNIPARC:UPI0000047764; GB:V00542; GB:J00214; NID:g32720; PIDN:CAA238
A;Note: a variant sequence differs from that shown in having 175-Phe, 182-Lys, and 184-G
R;Shirono, H.; Koga, J.; Uemura, H.; Matsuo, A.
Biosci. Biotechnol. Biochem. 58, 1714-1715, 1994
A;Title: Identification of glycosylated subtypes of interferon-alpha produced by human l
A;Reference number: PC2203; MUID:95036878; PMID:7765487
A;Accession: PC2203
A;Molecule type: protein
A;Residues: 'X',25-43 <SHI>
A;Cross-references: UNIPARC:UPI000017365E
A;Experimental source: leukocyte
C;Genetics:
A;Gene: GDB:IFNA14
A;Cross-references: GDB:136356; OMIM:147579
A;Map position: 9p22-9p22
C;Superfamily: interferon alpha
C;Keywords: antiviral; glycoprotein
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-189/Product: interferon alpha-I-14 #status experimental <MAT>
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F;24-122,52-162/Disulfide bonds: #status predicted
F;25,95/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             82.7%;  Score 793.5;  DB 1;  Length 189;
  Best Local Similarity   82.0%;  Pred. No. 4.7e-66;
  Matches  155;  Conservative   16;  Mismatches   17;  Indels    1;  Gaps    1;

Qy          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFG 60
              ||| |||::||:|||||||||:||:| ||||| :||||||:||||||| |||||||||
Db          1 MALPFALMMALVVLSCKSSCSLGCNLSQTHSLNNRRTLMLMAQMRRISPFSCLKDRHDFE 60

Qy         61 FPQEEF-GNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLE 119
              |||||| ||||||: | |||||:|| |||||||:||||||||||:||| ||:||:||||
Db         61 FPQEEFDGNQFQKAQAISVLHEMMQQTFNLFSTKNSSAAWDETLLEKFYIELFQQMNDLE 120

Qy        120 ACVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTN 179
              ||||| ||| ||||| |||||||:|||||||||| ||||||||||||||||||| | |||
Db        121 ACVIQEVGVEETPLMNEDSILAVKKYFQRITLYLMEKKYSPCAWEVVRAEIMRSLSFSTN 180

Qy        180 LQESLRSKE 188
              ||: || |:
Db        181 LQKRLRRKD 189


RESULT 6
I52347
interferon alpha-M1 precursor - human
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I52347
R;Linnane, A.W.; Beilharz, M.W.; McMullen, G.L.; Macreadie, I.G.; Murphy, M.; Nisbet, I.
Biochem. Int. 8, 725-732, 1984
A;Title: Nucleotide sequence and expression in E. coli of a human interferon-alpha gene
A;Reference number: I52347; MUID:84307815; PMID:6089830
A;Accession: I52347
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-189 <RES>
A;Cross-references: UNIPROT:P05014; UNIPARC:UPI000002BA77; GB:M27318; NID:g184617; PIDN:
C;Genetics:
A;Gene: IFNA
C;Superfamily: interferon alpha

  Query Match             81.4%;  Score 781.5;  DB 2;  Length 189;
  Best Local Similarity   81.5%;  Pred. No. 6e-65;
  Matches  154;  Conservative   17;  Mismatches   17;  Indels    1;  Gaps    1;

Qy          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFG 60
              |||:|:||:|:|||| || ||:||||||||||:|| |:||||| ||| ||||||||||
Db          1 MALSFSLLMAVLVLSYKSICSLGCDLPQTHSLGNRRALILLAQMGRISHFSCLKDRHDFG 60

Qy         61 FPQEEF-GNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLE 119
              ||:||| |:|||||: | |||||||| ||||||:||||||:::||:|| ||||||||||
Db         61 FPEEEFDGHQFQKAQAISVLHEMIQQTFNLFSTEDSSAAWEQSLLEKFSTELYQQLNDLE 120

Qy        120 ACVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTN 179
              ||||| ||| ||||| |||||||||||||||| |||||||||||||||||| | |||
Db        121 ACVIQEVGVEETPLMNEDSILAVRKYFQRITLYLTEKKYSPCAWEVVRAEIMRSLSFSTN 180

Qy        180 LQESLRSKE 188
              ||: || |:
Db        181 LQKRLRRKD 189


RESULT 7
I51970
interferon precursor - human
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 16-Jul-1999
C;Accession: I51970
R;Saveliev, V.I.; Zlochevsky, M.L.; Sorokin, A.V.; Naroditskaya, V.A.; Bolotin, A.P.; De
Antibiot. Med. Biotekhnol. 31, 592-596, 1986
A;Title: [Cloning and the determination of the nucleotide sequences in 2 genes of human
A;Reference number: I51970; MUID:87024453; PMID:3767336
A;Accession: I51970
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-189 <RES>
A;Cross-references: UNIPARC:UPI000016AB15; GB:M38289; NID:g186407; PIDN:AAA59165.1; PID:
C;Genetics:
A;Gene: IFNA
C;Superfamily: interferon alpha

  Query Match             81.2%;  Score 779.5;  DB 2;  Length 189;
  Best Local Similarity   81.0%;  Pred. No. 9.2e-65;
  Matches  153;  Conservative   17;  Mismatches   18;  Indels    1;  Gaps    1;

Qy          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFG 60
              |||:|:||:|:|||| || ||:||||||||||:|| |:||||| ||| ||||||||||
Db          1 MALSFSLLMAVLVLSYKSICSLGCDLPQTHSLGNRRALILLAQMGRISPFSCLKDRHDFG 60

Qy         61 FPQEEF-GNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLE 119
              |||||| |||||| : |||||||||| ||||||:||||||:::||:|| |||||||:||
Db         61 LPQEEFDGNQFQKTQAIPVLHEMIQQTFNLFSTEDSSAAWEQSLLEKFSTELYQQLNNLE 120

Qy        120 ACVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTN 179
              ||||| ||: ||||| |||||||||||||||| |||||||||||||||||| | |||
Db        121 ACVIQEVGMEETPLMNEDSILAVRKYFQRITLYLTEKKYSPCAWEVVRAEIMRSLSFSTN 180

Qy        180 LQESLRSKE 188
              ||: || |:
Db        181 LQKRLRRKD 189


RESULT 8
IVHUA1
interferon alpha-1 precursor - human
N;Alternate names: interferon alpha-13; interferon alpha-D; interferon alpha-I-1
C;Species: Homo sapiens (man)
C;Date: 22-May-1981 #sequence_revision 01-Sep-1981 #text_change 09-Jul-2004
C;Accession: C23285; A91467; A93226; A93249; I58213; S43715; S41196; A01826
R;Capon, D.J.; Shepard, H.M.; Goeddel, D.V.
Mol. Cell. Biol. 5, 768-779, 1985
A;Title: Two distinct families of human and bovine interferon-alpha genes are coordinate
A;Reference number: A93070; MUID:85187974; PMID:2985969
A;Accession: C23285
A;Molecule type: DNA
A;Residues: 1-189 <CAP>
A;Cross-references: UNIPROT:P01562; UNIPARC:UPI000002C6D3
R;Mantei, N.; Schwarzstein, M.; Streuli, M.; Panem, S.; Nagata, S.; Weissmann, C.
Gene 10, 1-10, 1980
A;Title: The nucleotide sequence of a cloned human leukocyte inteferon cDNA.
A;Reference number: A91467; MUID:81005094; PMID:6157600
A;Accession: A91467
A;Molecule type: mRNA
A;Residues: 1-189 <MAN>
A;Cross-references: UNIPARC:UPI000002C6D3; GB:V00537; NID:g32711; PIDN:CAA23798.1; PID:g
R;Taniguchi, T.; Mantei, N.; Schwarzstein, M.; Nagata, S.; Muramatsu, M.; Weissmann, C.
Nature 285, 547-549, 1980
A;Title: Human leukocyte and fibroblast interferons are structurally related.
A;Reference number: A93226; MUID:80254543; PMID:6157095
A;Accession: A93226
A;Molecule type: mRNA
A;Residues: 1-189 <TAN>
A;Cross-references: UNIPARC:UPI000002C6D3
R;Goeddel, D.V.; Leung, D.W.; Dull, T.J.; Gross, M.; Lawn, R.M.; McCandliss, R.; Seeburg
Nature 290, 20-26, 1981
A;Title: The structure of eight distinct cloned human leukocyte interferon cDNAs.
A;Reference number: A93249; MUID:81148795; PMID:6163083
A;Accession: A93249
A;Molecule type: mRNA
A;Residues: 1-136,'V',138-189 <GOE>
A;Cross-references: UNIPARC:UPI0000141F49; GB:V00538; NID:g32713; PIDN:CAA23799.1; PID:g
A;Note: eight classes of interferon alpha clones were identified; this sequence is deriv
R;Weber, H.; Weissmann, C.
Nucleic Acids Res. 11, 5661-5669, 1983
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A;Title: Formation of genes coding for hybrid proteins by recombination between related,
A;Reference number: I58213; MUID:83299241; PMID:6310510
A;Accession: I58213
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 24-189 <RES>
A;Cross-references: UNIPARC:UPI000002F8DA; GB:M29884; NID:g184583; PIDN:AAA52714.1; PID:
R;Henco, K.; Brosius, J.; Fujisawa, A.; Fujisawa, J.I.; Haynes, J.R.; Hochstadt, J.; Kov
J. Mol. Biol. 185, 227-260, 1985
A;Title: Structural relationship of human interferon alpha genes and pseudogenes.
A;Reference number: A92916; MUID:86037205; PMID:4057246
A;Accession: S43715
A;Molecule type: DNA
A;Residues: 1-189 <HEN>
A;Cross-references: UNIPARC:UPI000002C6D3; EMBL:X75934
R;Rostoks, N.
submitted to the EMBL Data Library, December 1993
A;Reference number: S41196
A;Accession: S41196
A;Molecule type: DNA
A;Residues: 1-9,'A',11-189 <ROS>
A;Cross-references: UNIPARC:UPI000002C35C; EMBL:X75934; NID:g439666; PIDN:CAA53538.1; PI
C;Genetics:
A;Gene: GDB:IFNA1
A;Cross-references: GDB:136353; OMIM:147660
A;Map position: 9p22-9p22
C;Superfamily: interferon alpha
C;Keywords: antiviral; cytokine; leukocyte
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-189/Product: interferon alpha-1 #status predicted <MAT>
F;24-122,52-162/Disulfide bonds: #status predicted

  Query Match             80.5%;  Score 772.5;  DB 1;  Length 189;
  Best Local Similarity   82.0%;  Pred. No. 4.1e-64;
  Matches  155;  Conservative   10;  Mismatches   23;  Indels    1;  Gaps    1;

Qy          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFG 60
              ||  ||||: |:|||||||||:|||||:|||| :|||||||||| |||  ||| ||||||
Db          1 MASPFALLMVLVVLSCKSSCSLGCDLPETHSLDNRRTLMLLAQMSRISPSSCLMDRHDFG 60

Qy         61 FPQEEF-GNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLE 119
              |||||| ||||||| | ||||:||||||||:|||||||||| ||||| ||||||||||
Db         61 FPQEEFDGNQFQKAPAISVLHELIQQIFNLFTTKDSSAAWDEDLLDKFCTELYQQLNDLE 120

Qy        120 ACVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTN 179
              |||:|    | |||||  ||||||:|||:|||||| |||||||||||||||||| |||||
Db        121 ACVMQEERVGETPLMNADSILAVKKYFRRITLYLTEKKYSPCAWEVVRAEIMRSLSLSTN 180

Qy        180 LQESLRSKE 188
              |||  ||  ||
Db        181 LQERLRRKE 189


RESULT 9
IVHU4B
interferon alpha-I-4b precursor - human
N;Alternate names: HuIFN-alpha-I-4b; type I interferon
C;Species: Homo sapiens (man)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 09-Jul-2004
C;Accession: E23753
R;Henco, K.; Brosius, J.; Fujisawa, A.; Fujisawa, J.I.; Haynes, J.R.; Hochstadt, J.; Kov
J. Mol. Biol. 185, 227-260, 1985
A;Title: Structural relationship of human interferon alpha genes and pseudogenes.
A;Reference number: A92916; MUID:86037205; PMID:4057246
A;Accession: E23753
A;Molecule type: DNA
A;Residues: 1-189 <HEN>
A;Cross-references: UNIPROT:P05014; UNIPARC:UPI0000047761; GB:X02955; NID:g32656; PIDN:C
C;Genetics:
A;Gene: GDB:IFN1@
A;Cross-references: GDB:119328; OMIM:147660
A;Map position: 9p22-9p22
C;Superfamily: interferon alpha
C;Keywords: antiviral
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-189/Product: interferon alpha-I-4b #status predicted <MAT>
F;24-122,52-162/Disulfide bonds: #status predicted

  Query Match             80.3%;  Score 770.5;  DB 1;  Length 189;
  Best Local Similarity   80.4%;  Pred. No. 6.3e-64;
  Matches  152;  Conservative   17;  Mismatches   19;  Indels    1;  Gaps    1;

Qy          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFG 60
              |||:|:||:|:|||| || ||:||||||||||:|| |:||||| ||| ||||||||||
Db          1 MALSFSLLMAVLVLSYKSICSLGCDLPQTHSLGNRRALILLAQMGRISHFSCLKDRHDFG 60

Qy         61 FPQEEF-GNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLE 119
              ||:||| |:|||| : | |||||||| |||||:|||||:::||:|| ||||||||||
Db         61 FPEEEFDGHQFQKTQAISVLHEMIQQTFNLFSTEDSSAAWEQSLLEKFSTELYQQLNDLE 120

Qy        120 ACVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTN 179
              |||||  ||| |||||  |||||||||||||||| |||||||||||||||||| | |||
Db        121 ACVIQEVGVEETPLMNVDSILAVRKYFQRITLYLTEKKYSPCAWEVVRAEIMRSLSFSTN 180

Qy        180 LQESLRSKE 188
              ||: || |:
Db        181 LQKRLRRKD 189


RESULT 10
I84464
interferon-alpha-F - human
C;Species: Homo sapiens (man)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
C;Accession: I84464; I37583
R;Gren, E.Y.; Berzin, V.M.; Tsimanis, A.Y.; Apsalon, U.R.; Vishnevskii, Y.I.; Yansone, I
.A.; Lozha, V.P.; Kavsan, V.M.; Efimov, V.A.; Sverdlov, E.D.
Dokl. Biochem. 269, 91-95, 1983
A;Title: A new type of leukocytic interferon.
A;Reference number: I37583
A;Accession: I84464
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-189 <RES>
A;Cross-references: UNIPROT:P01568; UNIPARC:UPI000002C35A; GB:M12350; NID:g184598; PIDN:
A;Accession: I37583
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-189 <RE2>
A;Cross-references: UNIPARC:UPI000002C35A; EMBL:X00145; NID:g32724; PIDN:CAA24980.1; PII
C;Genetics:
A;Gene: IFNA
C;Superfamily: interferon alpha

  Query Match             80.1%;  Score 768.5;  DB 2;  Length 189;
  Best Local Similarity   81.5%;  Pred. No. 9.6e-64;
  Matches  154;  Conservative   13;  Mismatches   21;  Indels    1;  Gaps    1;

Qy          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFG 60
              |||:|:||:|:|||| || ||:||||||||||:|| |:||||| ||| ||||||||||
Db          1 MALSFSLLMAVLVLSYKSICSLGCDLPQTHSLGNRRALILLAQMGRISPFSCLKDRHDFG 60

Qy         61 FPQEEF-GNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLE 119
              |||||| ||||||: | |||||||| |||||||||| |:::||:|| ||| |||||||
Db         61 FPQEEFDGNQFQKAQAISVLHEMIQQTFNLFSTKDSSATWEQSLLEKFSTELNQQLNDLE 120

Qy        120 ACVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTN 179
              |||||  ||| |||||  |||||||:|||||||||| ||||||||||||||||||||||
Db        121 ACVIQEVGVEETPLMNVDSILAVKKYFQRITLYLTEKKYSPCAWEVVRAEIMRSFSLSKI 180

Qy        180 LQESLRSKE 188
              || || ||
Db        181 FQERLRRKE 189


RESULT 11
```

```
IVHU16
interferon alpha-I-16 precursor - human
N;Alternate names: HuIFN-alpha-I-16; interferon alpha-I-WA; type I interferon
C;Species: Homo sapiens (man)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 09-Jul-2004
C;Accession: G23753; A22068; I73334
R;Henco, K.; Brosius, J.; Fujisawa, A.; Fujisawa, J.I.; Haynes, J.R.; Hochstadt, J.; Kov
J. Mol. Biol. 185, 227-260, 1985
A;Title: Structural relationship of human interferon alpha genes and pseudogenes.
A;Reference number: A92916; MUID:86037205; PMID:4057246
A;Accession: G23753
A;Molecule type: DNA
A;Residues: 1-189 <HEN>
A;Cross-references: UNIPROT:P05015; UNIPARC:UPI0000047763; GB:X02957; NID:g32653; PIDN:C
R;Torczynski, R.M.; Fuke, M.; Bollon, A.P.
Proc. Natl. Acad. Sci. U.S.A. 81, 6451-6455, 1984
A;Title: Human genomic library screened with 17-base oligonucleotide probes yields a nov
A;Reference number: A22068; MUID:85038533; PMID:6387705
A;Accession: A22068
A;Molecule type: DNA
A;Residues: 1-189 <TOR>
A;Cross-references: UNIPARC:UPI0000047763; GB:K02055; NID:g184620; PIDN:AAA52727.1; PID:
R;Gren, E.; Berzin, V.M.; Jansone, I.; Tsimanis, A.; Vishnevsky, Y.; Apsalons, U.
J. Interferon Res. 4, 609-617, 1984
A;Title: Novel human leukocyte interferon subtype and structural comparison of alpha int
A;Reference number: I56313; MUID:85056523; PMID:6548765
A;Accession: I73334
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-189 <RES>
A;Cross-references: UNIPARC:UPI0000047763; GB:M28585; NID:g184643; PIDN:AAA36042.1; PID:
C;Genetics:
A;Gene: GDB:IFNA16
A;Cross-references: GDB:136357; OMIM:147580
A;Map position: 9p22-9p22
A;Introns: #status absent
C;Superfamily: interferon alpha
C;Keywords: antiviral; cytokine; leukocyte
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-189/Product: interferon alpha-I-16 #status predicted <MAT>
F;24-122,52-162/Disulfide bonds: #status predicted

  Query Match             79.9%;  Score 767.5;  DB 1;  Length 189;
  Best Local Similarity   81.0%;  Pred. No. 1.2e-63;
  Matches  153;  Conservative   12;  Mismatches   23;  Indels    1;  Gaps    1;

Qy          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFG 60
              |||:|:||:|:|||| || ||:|||||||||||:|| |:||||| ||| |||||||:|||
Db          1 MALSFSLLMAVLVLSYKSICSLGCDLPQTHSLGNRRALILLAQMGRISHFSCLKDRYDFG 60

Qy         61 FPQEEF-GNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLE 119
              |||| | |||||||: |   |||||| ||||||||||||||||||||||| ||:|||||||
Db         61 FPQEVFDGNQFQKAQAISAFHEMIQQTFNLFSTKDSSAAWDETLLDKFYIELFQQLNDLE 120

Qy        120 ACVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTN 179
              ||| | ||| |  || ||||||||||||||||||  |||||||||||||||||||| |||
Db        121 ACVTQEVGVEEIALMNEDSILAVRKYFQRITLYLMGKKYSPCAWEVVRAEIMRSFSFSTN 180

Qy        180 LQESLRSKE 188
              ||: || |:
Db        181 LQKGLRRKD 189


RESULT 12
IVHUA5
interferon alpha-5 precursor - human
C;Species: Homo sapiens (man)
C;Date: 01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change 09-Jul-2004
C;Accession: A60937; A01830
R;Bartholomew, C.; Windass, J.D.
J. Interferon Res. 9, 407-417, 1989
A;Title: Identification of a functional allele of a human interferon-alpha gene previous
A;Reference number: A60937; MUID:89328015; PMID:2526839
A;Accession: A60937
A;Molecule type: DNA
A;Residues: 1-189 <BAR>
A;Cross-references: UNIPROT:P01566; UNIPARC:UPI0000047765
A;Note: this genomic sequence, SMTIII.1A, encodes a functional allele for alpha interfe
ence and is a pseudogene
R;Goeddel, D.V.; Leung, D.W.; Dull, T.J.; Gross, M.; Lawn, R.M.; McCandliss, R.; Seebur
Nature 290, 20-26, 1981
A;Title: The structure of eight distinct cloned human leukocyte interferon cDNAs.
A;Reference number: A93249; MUID:81148795; PMID:6163083
A;Accession: A01830
A;Molecule type: mRNA
A;Residues: 1-189 <GOE>
A;Cross-references: UNIPARC:UPI0000047765; GB:V00551; GB:J00209; NID:g32748; PIDN:CAA23
A;Note: eight classes of interferon alpha clones were identified; this sequence is deri
C;Genetics:
A;Gene: GDB:IFNA5
A;Cross-references: GDB:136362; OMIM:147565
A;Map position: 9p22-9p22
C;Superfamily: interferon alpha
C;Keywords: leukocyte
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-189/Product: interferon alpha-5 #status predicted <MAT>
F;24-122,52-162/Disulfide bonds: #status predicted

  Query Match             79.8%;  Score 766.5;  DB 1;  Length 189;
  Best Local Similarity   80.4%;  Pred. No. 1.5e-63;
  Matches  152;  Conservative   16;  Mismatches   20;  Indels    1;  Gaps    1;

Qy          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFG 60
              |||:|:||:|:|||| || ||:|||||||||||:|| |:||||| ||| |||||||:|||
Db          1 MALSFSLLMAVLVLSYKSICSLGCDLPQTHSLGNRRALILLGQMGRISPFSCLKDRHDFR 60

Qy         61 FPQEEF-GNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLE 119
              ||||| ||||||: | |||||||| ||||||:||||||:::||:|| ||||||||||
Db         61 IPQEEFDGNQFQKAQAISVLHEMIQQTFNLFSTEDSSAAWEQSLLEKFSTELYQQLNDLE 120

Qy        120 ACVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTN 179
              ||||| ||| ||||| |||||||||||||||||| |:|||||||||||||||| | |||
Db        121 ACVIQEVGVEETPLMNEDSILAVRKYFQRITLYLIERKYSPCAWEVVRAEIMRSLSFSTN 180

Qy        180 LQESLRSKE 188
              ||: || |:
Db        181 LQKRLRRKD 189


RESULT 13
IVHUF
interferon alpha-I-F precursor - human
N;Alternate names: HuIFN-alpha-I-F; LeIF F; type I interferon
C;Species: Homo sapiens (man)
C;Date: 01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change 09-Jul-2004
C;Accession: A01832
R;Goeddel, D.V.; Leung, D.W.; Dull, T.J.; Gross, M.; Lawn, R.M.; McCandliss, R.; Seebur
Nature 290, 20-26, 1981
A;Title: The structure of eight distinct cloned human leukocyte interferon cDNAs.
A;Reference number: A93249; MUID:81148795; PMID:6163083
A;Accession: A01832
A;Molecule type: mRNA
A;Residues: 1-189 <GOE>
A;Cross-references: UNIPROT:P01568; UNIPARC:UPI0000047762; GB:V00540; GB:J00212; NID:g3
A;Note: eight classes of interferon alpha clones were identified; this sequence is deri
C;Genetics:
A;Gene: GDB:IFN1@
A;Cross-references: GDB:119328; OMIM:147660
A;Map position: 9p22-9p22
C;Superfamily: interferon alpha
C;Keywords: antiviral
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-189/Product: interferon alpha-I-F #status predicted <MAT>
F;24-122,52-162/Disulfide bonds: #status predicted

  Query Match             79.8%;  Score 766.5;  DB 1;  Length 189;
```

```
  Best Local Similarity   81.0%;  Pred. No. 1.5e-63;
  Matches  153;  Conservative   14;  Mismatches   21;  Indels    1;  Gaps    1;

Qy          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFG 60
              |||:|:||:|:|||| || ||:||||||||||:|| |:||||| ||| ||||||||||
Db          1 MALSFSLLMAVLVLSYKSICSLGCDLPQTHSLGNRRALILLAQMGRISPFSCLKDRHDFG 60

Qy         61 FPQEEF-GNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLE 119
              |||||| ||||||: | |||||||| |||||||||| |:::||:|| ||| |||||:|
Db         61 FPQEEFDGNQFQKAQAISVLHEMIQQTFNLFSTKDSSATWEQSLLEKFSTELNQQLNDME 120

Qy        120 ACVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTN 179
              ||||| ||| |||||  ||||||:|||||||||| ||||||||||||||||||||||
Db        121 ACVIQEVGVEETPLMNVDSILAVKKYFQRITLYLTEKKYSPCAWEVVRAEIMRSFSLSKI 180

Qy        180 LQESLRSKE 188
                || || ||
Db        181 FQERLRRKE 189


RESULT 14
IVHUA9
interferon alpha-17 precursor - human
N;Alternate names: interferon alpha-9; interferon alpha-I'
C;Species: Homo sapiens (man)
C;Date: 01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change 09-Jul-2004
C;Accession: A01835; A22255; C42753
R;Lawn, R.M.; Adelman, J.; Dull, T.J.; Gross, M.; Goeddel, D.; Ullrich, A.
Science 212, 1159-1162, 1981
A;Title: DNA sequence of two closely linked human leukocyte interferon genes.
A;Reference number: A94255; MUID:81201124; PMID:6165082
A;Accession: A01835
A;Molecule type: DNA
A;Residues: 1-189 <LAW>
A;Cross-references: UNIPROT:P01571; UNIPARC:UPI0000141F4B; GB:J00216; GB:V00532; NID:g32
R;Mizoguchi, J.; Pitha, P.M.; Raj, N.B.K.
DNA 4, 221-232, 1985
A;Title: Efficient expression in Escherichia coli of two species of human interferon-alp
A;Reference number: A22255; MUID:85229953; PMID:3891272
A;Accession: A22255
A;Molecule type: mRNA
A;Residues: 1-56,'H',58-189 <MIZ>
A;Cross-references: UNIPARC:UPI0000052AF9; GB:M11026; NID:g184612; PIDN:AAA52725.1; PID:
R;Zoon, K.C.; Miller, D.; Bekisz, J.; zur Nedden, D.; Enterline, J.C.; Nguyen, N.Y.; Hu,
J. Biol. Chem. 267, 15210-15216, 1992
A;Title: Purification and characterization of multiple components of human lymphoblastoi
A;Reference number: A42753; MUID:92340576; PMID:1634550
A;Accession: C42753
A;Molecule type: protein
A;Residues: 'X',25-50,'XX',53-56 <ZOO>
A;Cross-references: UNIPARC:UPI000017365F
C;Genetics:
A;Gene: GDB:IFNA17
A;Cross-references: GDB:136358; OMIM:147583
A;Map position: 9p22-9p22
C;Superfamily: interferon alpha
C;Keywords: leukocyte
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-189/Product: interferon alpha-17 #status predicted <MAT>
F;24-122,52-162/Disulfide bonds: #status predicted

  Query Match             79.2%;  Score 760.5;  DB 1;  Length 189;
  Best Local Similarity   79.9%;  Pred. No. 5.3e-63;
  Matches  151;  Conservative   17;  Mismatches   20;  Indels    1;  Gaps    1;

Qy          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFG 60
              |||:|:||:|:|||| || ||:||||||||||:|| |:||||| ||| ||||||| |||
Db          1 MALSFSLLMAVLVLSYKSICSLGCDLPQTHSLGNRRALILLAQMGRISPFSCLKDRPDFG 60

Qy         61 FPQEEF-GNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLE 119
              ||||| |||||| : | |||||||| |||||:||||||:::||:|| |||||||||:||
Db         61 LPQEEFDGNQFQKTQAISVLHEMIQQTFNLFSTEDSSAAWEQSLLEKFSTELYQQLNNLE 120

Qy        120 ACVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTN 179
              ||||| ||| |||||  ||||||:|||||||||| ||||||||||||||||||||||
Db        121 ACVIQEVGVEETPLMNEDSILAVRKYFQRITLYLTEKKYSPCAWEVVRAEIMRSLSFSTN 180

Qy        180 LQESLRSKE 188
              ||: || |:
Db        181 LQKILRRKD 189


RESULT 15
I37584
IFN-alpha-N-protein - human
C;Species: Homo sapiens (man)
C;Date: 04-Oct-1996 #sequence_revision 04-Oct-1996 #text_change 09-Jul-2004
C;Accession: I37584
R;Gren, E.Y.; Berzin, V.M.; Tsimanis, A.Y.; Apsalon, U.R.; Vishnevskii, Y.I.; Yansone, I
.A.; Lozha, V.P.; Kavsan, V.M.; Efimov, V.A.; Sverdlov, E.D.
Dokl. Biochem. 269, 91-95, 1983
A;Title: A new type of leukocytic interferon.
A;Reference number: I37583
A;Accession: I37584
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-189 <RES>
A;Cross-references: UNIPROT:Q14618; UNIPARC:UPI0000072A39; EMBL:X00140; NID:g32726; PIDN
C;Superfamily: interferon alpha

  Query Match             78.8%;  Score 756.5;  DB 2;  Length 189;
  Best Local Similarity   79.9%;  Pred. No. 1.2e-62;
  Matches  151;  Conservative   12;  Mismatches   25;  Indels    1;  Gaps    1;

Qy          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFG 60
              | |:|:||:|:|||| || ||:||||||||||:||  :||||| ||| |||||||:|||
Db          1 MPLSFSLLMAVLVLSYKSICSLGCDLPQTHSLGNRRAWILLAQMGRISHFSCLKDRYDFG 60

Qy         61 FPQEEF-GNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLE 119
              |||| | |||||||: |   |||||| ||||||||||||||||||||| ||:|||||||
Db         61 FPQEVFDGNQFQKAQAISAFHEMIQQTFNLFSTKDSSAAWDETLLDKFYIELFQQLNDLE 120

Qy        120 ACVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTN 179
              ||| | ||| |  || |||||||||||||||  |||||||||||||||||| |||
Db        121 ACVTQEVGVEEIALMNEDSILAVRKYFQRITLYLMGKKYSPCAWEVVRAEIMRSFSFSTN 180

Qy        180 LQESLRSKE 188
              ||: || |:
Db        181 LQKGLRRKD 189


Search completed: October 14, 2006, 08:02:36
Job time : 42 secs
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GenCore version 5.1.9

OM protein - protein search, using sw model

Run on: October 14, 2006, 07:53:27 ; Search time 301 Seconds
(without alignments)
577.751 Million cell updates/sec

Title: US-10-653-350-1
Perfect score: 960
Sequence: 1 MALTFALLVALLVLSCKSSC.....EIMRSFSLSTNLQESLRSKE 188

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	960	100.0	188	2	Q6DJX8_HUMAN	Q6djx8 homo sapien
2	957	99.7	188	1	IFNA2_HUMAN	P01563 homo sapien
3	851	88.6	166	2	Q86UP4_HUMAN	Q86up4 homo sapien
4	814.5	84.8	189	2	Q95J78_SAGOE	Q95j78 saguinus oe
5	809.5	84.3	189	1	IFNA5_HUMAN	P01569 homo sapien
6	809.5	84.3	189	2	Q52LX3_HUMAN	Q52lx3 homo sapien
7	808.5	84.2	189	1	IFNA6_HUMAN	P05013 homo sapien
8	808.5	84.2	189	2	Q5VYQ1_HUMAN	Q5vyq1 homo sapien
9	793.5	82.7	189	1	IFN14_HUMAN	P01570 homo sapien
10	793.5	82.7	189	2	Q5VZ56_HUMAN	Q5vz56 homo sapien
11	789.5	82.2	189	2	Q95J77_SAGOE	Q95j77 saguinus oe
12	786	81.9	154	2	Q6QNB6_HUMAN	Q6qnb6 homo sapien
13	781.5	81.4	189	1	IFNA4_HUMAN	P05014 homo sapien
14	781.5	81.4	189	2	Q5VV15_HUMAN	Q5vv15 homo sapien
15	776.5	80.9	189	2	Q52LB8_HUMAN	Q52lb8 homo sapien
16	772.5	80.5	189	1	IFNA1_HUMAN	P01562 homo sapien
17	772.5	80.5	189	2	Q2M1L8_HUMAN	Q2m118 homo sapien
18	770.5	80.3	189	1	IFN17_HUMAN	P01571 homo sapien
19	770.5	80.3	189	2	Q5VZ53_HUMAN	Q5vz53 homo sapien
20	768.5	80.1	189	1	IFN21_HUMAN	P01568 homo sapien
21	768.5	80.1	189	2	Q5VWD1_HUMAN	Q5vwd1 homo sapien
22	767.5	79.9	189	1	IFN16_HUMAN	P05015 homo sapien
23	767.5	79.9	189	2	Q5VV12_HUMAN	Q5vv12 homo sapien
24	766.5	79.8	189	1	IFN10_HUMAN	P01566 homo sapien
25	766.5	79.8	189	2	Q5VV13_HUMAN	Q5vv13 homo sapien
26	760.5	79.2	174	2	Q8MJT1_SAISC	Q8mjt1 saimiri sci
27	756.5	78.8	189	2	Q14618_HUMAN	Q14618 homo sapien
28	754.5	78.6	189	1	IFNA8_HUMAN	P32881 homo sapien
29	754.5	78.6	189	2	Q5VYQ3_HUMAN	Q5vyq3 homo sapien
30	744.5	77.6	189	1	IFNA7_HUMAN	P01567 homo sapien
31	744.5	77.6	189	2	Q5VV14_HUMAN	Q5vv14 homo sapien
32	739.5	77.0	181	2	Q14608_HUMAN	Q14608 homo sapien
33	722.5	75.3	184	1	IFNA4_HORSE	P05006 equus cabal
34	718.5	74.8	184	1	IFNA2_HORSE	P05004 equus cabal
35	710.5	74.0	184	1	IFNA3_HORSE	P05005 equus cabal
36	704.5	73.4	184	1	IFNA1_HORSE	P05003 equus cabal
37	677.5	70.6	166	2	Q8WZ68_HUMAN	Q8wz68 homo sapien
38	640.5	66.7	189	1	IFNA1_PIG	P49879 sus scrofa
39	637.5	66.4	189	2	Q304W3_PIG	Q304w3 sus scrofa
40	637.5	66.4	189	2	Q6VAB8_PIG	Q6vab8 sus scrofa
41	631.5	65.8	189	2	Q304V9_PIG	Q304v9 sus scrofa
42	625.5	65.2	181	2	Q304W4_PIG	Q304w4 sus scrofa
43	622.5	64.8	189	2	Q304W5_PIG	Q304w5 sus scrofa
44	616.5	64.2	181	2	Q304W0_PIG	Q304w0 sus scrofa
45	611.5	63.7	189	2	Q68IQ5_PIG	Q68iq5 sus scrofa

ALIGNMENTS

RESULT 1
Q6DJX8_HUMAN
ID Q6DJX8_HUMAN PRELIMINARY; PRT; 188 AA.
AC Q6DJX8;
DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 10-MAY-2005, sequence version 1.
DT 21-FEB-2006, entry version 13.
DE Interferon, alpha 2 (IFNA2 protein).
GN Name=IFNA2; ORFNames=RP11-354P17.2-001;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=PCR rescued clones, and Pooled tissue;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Pooled tissue;
RG NIH MGC Project;
RL Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Halleck A., Ebert L., Mkoundinya M., Schick M., Eisenstein S.,
RA Neubert P., Kstrang K., Schatten R., Shen B., Henze S., Mar W.,
RA Korn B., Zuo D., Hu Y., LaBaer J.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE.
RA Beasley H.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
RN [5]

```
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=PCR rescued clones;
RG   NIH MGC Project;
RL   Submitted (SEP-2005) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: Secreted protein (By similarity).
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; BC074937; AAH74937.1; -; mRNA.
DR   EMBL; CR541921; CAG46719.1; -; mRNA.
DR   EMBL; AL353732; CAH72906.1; -; Genomic_DNA.
DR   EMBL; BC104164; AAI04165.1; -; mRNA.
DR   EMBL; BC074936; AAH74936.1; -; mRNA.
DR   EMBL; BC104163; AAI04164.1; -; mRNA.
DR   SMR; Q6DJX8; 24-188.
DR   Ensembl; ENSG00000188379; Homo sapiens.
DR   GO; GO:0005615; C:extracellular space; IEA.
DR   GO; GO:0005126; F:hematopoietin/interferon-class (D200-domain. . .; IEA.
DR   GO; GO:0006952; P:defense response; IEA.
DR   GO; GO:0009615; P:response to virus; IEA.
DR   InterPro; IPR000471; Interferon_abd.
DR   PANTHER; PTHR11691; Interferon_abd; 1.
DR   Pfam; PF00143; Interferon; 1.
DR   PRINTS; PR00266; INTERFERONAB.
DR   SMART; SM00076; IFabd; 1.
DR   PROSITE; PS00252; INTERFERON_A_B_D; 1.
KW   Antiviral defense; Cytokine.
SQ   SEQUENCE   188 AA;  21578 MW;  9BAA221D2BFB421D CRC64;

  Query Match           100.0%;  Score 960;  DB 2;  Length 188;
  Best Local Similarity  100.0%;  Pred. No. 6.5e-78;
  Matches  188;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFG 60

Qy         61 FPQEEFGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FPQEEFGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEA 120

Qy        121 CVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNL 180

Qy        181 QESLRSKE 188
              ||||||||
Db        181 QESLRSKE 188


RESULT 2
IFNA2_HUMAN
ID   IFNA2_HUMAN     STANDARD;      PRT;   188 AA.
AC   P01563; P01564; Q14606; Q96KI6;
DT   21-JUL-1986, integrated into UniProtKB/Swiss-Prot.
DT   21-JUL-1986, sequence version 1.
DT   07-FEB-2006, entry version 67.
DE   Interferon alpha-2 precursor (Interferon alpha-A) (LeIF A).
GN   Name=IFNA2;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=81052322; PubMed=6159538;
RA   Goeddel D.V., Yelverton E., Ullrich A., Heyneker H.L., Miozzari G.,
RA   Holmes W., Seeburg P.H., Dull T.J., May L., Stebbing N., Crea R.,
RA   Maeda S., McCandliss R., Sloma A., Tabor J.M., Gross M.,
RA   Familletti P.C., Pestka S.;
RT   "Human leukocyte interferon produced by E. coli is biologically
RT   active.";
RL   Nature 287:411-416(1980).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=81148795; PubMed=6163083;
RA   Goeddel D.V., Leung D.W., Dull T.J., Gross M., Lawn R.M.,
RA   McCandliss R., Seeburg P.H., Ullrich A., Yelverton E., Gray P.W.;
RT   "The structure of eight distinct cloned human leukocyte interferon
RT   cDNAs.";
RL   Nature 290:20-26(1981).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=82060261; PubMed=6170983;
RA   Lawn R.M., Gross M., Houck C.M., Franke A.E., Gray P.V., Goeddel D.V.;
RT   "DNA sequence of a major human leukocyte interferon gene.";
RL   Proc. Natl. Acad. Sci. U.S.A. 78:5435-5439(1981).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Bone marrow tumor;
RX   MEDLINE=86069501; PubMed=3906813;
RA   Oliver G., Balbas P., Valle F., Soberon X., Bolivar F.;
RT   "Cloning of human leukocyte interferon cDNA and a strategy for its
RT   production in E. coli.";
RL   Rev. Latinoam. Microbiol. 27:141-150(1985).
RN   [5]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Placenta;
RX   MEDLINE=98357449; PubMed=9694076;
RA   Austruy E., Bagnis C., Carbuccia N., Maroc C., Birg F., Dubreuil P.,
RA   Mannoni P., Chabannon C.;
RT   "A defective retroviral vector encoding human interferon alpha 2 can
RT   transduce human leukemic cell lines.";
RL   Cancer Gene Ther. 5:247-256(1998).
RN   [6]
RP   NUCLEOTIDE SEQUENCE OF 7-188.
RX   MEDLINE=81015442; PubMed=6158094;
RA   Streuli M., Nagata S., Weissmann C.;
RT   "At least three human type alpha interferons: structure of alpha 2.";
RL   Science 209:1343-1347(1980).
RN   [7]
RP   NUCLEOTIDE SEQUENCE OF 24-188.
RX   MEDLINE=83299241; PubMed=6310510;
RA   Weber H., Weissmann C.;
RT   "Formation of genes coding for hybrid proteins by recombination
RT   between related, cloned genes in E. coli.";
RL   Nucleic Acids Res. 11:5661-5669(1983).
RN   [8]
RP   PROTEIN SEQUENCE OF 24-112 AND 136-188.
RX   MEDLINE=81052321; PubMed=6159537;
RA   Allen G., Fantes K.H.;
RT   "A family of structural genes for human lymphoblastoid (leukocyte-
RT   type) interferon.";
RL   Nature 287:408-411(1980).
RN   [9]
RP   PROTEIN SEQUENCE OF 24-58.
RX   MEDLINE=98087498; PubMed=9425112;
RA   Nyman T.A., Toeloe H., Parkkinen J., Kalkkinen N.;
RT   "Identification of nine interferon-alpha subtypes produced by Sendai
RT   virus-induced human peripheral blood leucocytes.";
RL   Biochem. J. 329:295-302(1998).
RN   [10]
RP   DISULFIDE BONDS.
RX   MEDLINE=81123083; PubMed=6162107;
RA   Wetzel R.;
RT   "Assignment of the disulphide bonds of leukocyte interferon.";
RL   Nature 289:606-607(1981).
RN   [11]
RP   CARBOHYDRATE-LINKAGE SITE THR-129, AND VARIANTS ALPHA-2B AND ALPHA-2C.
RX   MEDLINE=91264809; PubMed=2049076;
RA   Adolf G.R., Kalsner I., Ahorn H., Maurer-Fogy I., Cantell K.;
RT   "Natural human interferon-alpha 2 is O-glycosylated.";
RL   Biochem. J. 276:511-518(1991).
RN   [12]
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RP   POLYMORPHISM.
RX   MEDLINE=95353982; PubMed=7627809;
RA   Lee N., Ni D., Brissette R., Chou M., Hussain M., Gill D.S.,
RA   Liao M.-J., Testa D.;
RT   "Interferon-alpha 2 variants in the human genome.";
RL   J. Interferon Cytokine Res. 15:341-349(1995).
RN   [13]
RP   3D-STRUCTURE MODELING.
RX   MEDLINE=94052087; PubMed=8234245; DOI=10.1002/prot.340170109;
RA   Murgolo N.J., Windsor W.T., Hruza A., Reichert P., Tsarbopoulos A.,
RA   Baldwin S., Huang E., Pramanik B., Ealick S., Trotta P.P.;
RT   "A homology model of human interferon alpha-2.";
RL   Proteins 17:62-74(1993).
RN   [14]
RP   X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
RX   MEDLINE=97148339; PubMed=8994971; DOI=10.1016/S0969-2126(96)00152-9;
RA   Radhakrishnan R., Walter L.J., Hruza A., Reichert P., Trotta P.P.,
RA   Nagabhushan T.L., Walter M.R.;
RT   "Zinc mediated dimer of human interferon-alpha 2b revealed by X-ray
RT   crystallography.";
RL   Structure 4:1453-1463(1996).
RN   [15]
RP   STRUCTURE BY NMR.
RX   MEDLINE=98118493; PubMed=9417943; DOI=10.1006/jmbi.1997.1396;
RA   Klaus W., Gsell B., Labhardt A.M., Wipf B., Senn H.;
RT   "The three-dimensional high resolution structure of human interferon
RT   alpha-2a determined by heteronuclear NMR spectroscopy in solution.";
RL   J. Mol. Biol. 274:661-675(1997).
CC   -!- FUNCTION: Produced by macrophages, IFN-alpha have antiviral
CC       activities. Interferon stimulates the production of two enzymes: a
CC       protein kinase and an oligoadenylate synthetase.
CC   -!- SUBCELLULAR LOCATION: Secreted protein.
CC   -!- POLYMORPHISM: Three forms exist; alpha-2a (shown here), alpha-2b
CC       and alpha-2c.
CC   -!- PHARMACEUTICAL: Available under the names Roferon-A (Roche) or
CC       Intron-A (Schering-Plough). Used as an anticancer drug for its
CC       antiproliferative activity.
CC   -!- SIMILARITY: Belongs to the alpha/beta interferon family.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; J00207; AAB59402.1; -; Genomic_DNA.
DR   EMBL; V00544; CAA23805.1; -; mRNA.
DR   EMBL; V00548; CAA23809.1; -; mRNA.
DR   EMBL; V00549; CAA23810.1; -; mRNA.
DR   EMBL; Y11834; CAA72532.1; -; Genomic_DNA.
DR   EMBL; M54886; AAA59181.1; -; mRNA.
DR   EMBL; M29883; AAA52715.1; -; Genomic_DNA.
DR   EMBL; A04970; CAA00410.1; -; Unassigned_DNA.
DR   PIR; A93234; IVHUA2.
DR   PIR; I78570; I78570.
DR   PDB; 1ITF; NMR; @=24-188.
DR   PDB; 1RH2; X-ray; A/B/C/D/E/F=24-188.
DR   PDB; 2HIE; Model; @=24-188.
DR   GlycoSuiteDB; P01563; -.
DR   Ensembl; ENSG00000188379; Homo sapiens.
DR   HGNC; HGNC:5423; IFNA2.
DR   MIM; 147562; gene.
DR   LinkHub; P01563; -.
DR   GO; GO:0005132; F:interferon-alpha/beta receptor binding; TAS.
DR   GO; GO:0007166; P:cell surface receptor linked signal transdu. . .; TAS.
DR   GO; GO:0007267; P:cell-cell signaling; TAS.
DR   GO; GO:0006917; P:induction of apoptosis; TAS.
DR   GO; GO:0006954; P:inflammatory response; TAS.
DR   InterPro; IPR000471; Interferon_abd.
DR   PANTHER; PTHR11691; Interferon_abd; 1.
DR   Pfam; PF00143; Interferon; 1.
DR   PRINTS; PR00266; INTERFERONAB.
DR   ProDom; PD000550; Interferon_abd; 1.
DR   SMART; SM00076; IFabd; 1.
DR   PROSITE; PS00252; INTERFERON_A_B_D; 1.
KW   3D-structure; Antiviral defense; Cytokine; Direct protein sequencing;
KW   Glycoprotein; Pharmaceutical; Polymorphism; Signal.
FT   SIGNAL        1     23
FT   CHAIN        24    188       Interferon alpha-2.
FT                                 /FTId=PRO_0000016360.
FT   CARBOHYD    129    129       O-linked (GalNAc. . .).
FT                                 /FTId=CAR_000049.
FT   DISULFID     24    121
FT   DISULFID     52    161
FT   VARIANT      46     46       K -> R (in alpha-2B and alpha-2C).
FT                                 /FTId=VAR_004012.
FT   VARIANT      57     57       H -> R (in alpha-2C).
FT                                 /FTId=VAR_013001.
FT   HELIX        33     44
FT   TURN         49     54
FT   HELIX        63     66
FT   HELIX        76     91
FT   HELIX        93     98
FT   HELIX       101    123
FT   TURN        126    127
FT   TURN        133    133
FT   HELIX       134    155
FT   TURN        156    157
FT   HELIX       160    178
FT   TURN        179    182
SQ   SEQUENCE   188 AA;  21550 MW;  101DD21D394CBF97 CRC64;

  Query Match             99.7%;  Score 957;  DB 1;  Length 188;
  Best Local Similarity   99.5%;  Pred. No. 1.2e-77;
  Matches  187;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFG 60
              |||||||||||||||||||||||||||||||||||||||||||||||:|||||||||||||||
Db          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRKISLFSCLKDRHDFG 60

Qy         61 FPQEEFGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FPQEEFGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEA 120

Qy        121 CVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNL 180

Qy        181 QESLRSKE 188
              ||||||||
Db        181 QESLRSKE 188


RESULT 3
Q86UP4_HUMAN
ID   Q86UP4_HUMAN   PRELIMINARY;   PRT;   166 AA.
AC   Q86UP4;
DT   01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT   01-JUN-2003, sequence version 1.
DT   21-FEB-2006, entry version 13.
DE   Interferon alpha 2b.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Chikara S.K., Joseph B., Sharma G.;
RL   Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: Secreted protein (By similarity).
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AY255838; AAP20099.1; -; mRNA.
DR   HSSP; P01563; 1ITF.
DR   SMR; Q86UP4; 2-166.
DR   Ensembl; ENSG00000188379; Homo sapiens.
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DR   GO; GO:0005615; C:extracellular space; IEA.
DR   GO; GO:0005126; F:hematopoietin/interferon-class (D200-domain. . .; IEA.
DR   GO; GO:0006952; P:defense response; IEA.
DR   GO; GO:0009615; P:response to virus; IEA.
DR   InterPro; IPR000471; Interferon_abd.
DR   PANTHER; PTHR11691; Interferon_abd; 1.
DR   Pfam; PF00143; Interferon; 1.
DR   PRINTS; PR00266; INTERFERONAB.
DR   ProDom; PD000550; Interferon_abd; 1.
DR   SMART; SM00076; IFabd; 1.
DR   PROSITE; PS00252; INTERFERON_A_B_D; 1.
KW   Antiviral defense; Cytokine.
SQ   SEQUENCE   166 AA;  19400 MW;  B7DAC3C9E67782C6 CRC64;

  Query Match             88.6%;  Score 851;  DB 2;  Length 166;
  Best Local Similarity   100.0%;  Pred. No. 3.4e-68;
  Matches  165;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         24 CDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFGFPQEEFGNQFQKAETIPVLHEMI 83
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 CDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFGFPQEEFGNQFQKAETIPVLHEMI 61

Qy         84 QQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEACVIQGVGVTETPLMKEDSILAVR 143
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 QQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEACVIQGVGVTETPLMKEDSILAVR 121

Qy        144 KYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNLQESLRSKE 188
              ||||||||||||||||||||||||||||||||||||||||||||||
Db        122 KYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNLQESLRSKE 166


RESULT 4
Q95J78_SAGOE
ID   Q95J78_SAGOE   PRELIMINARY;   PRT;   189 AA.
AC   Q95J78;
DT   01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT   01-DEC-2001, sequence version 1.
DT   21-FEB-2006, entry version 18.
DE   Interferon-alpha precursor.
GN   Name=ifn-alpha;
OS   Saguinus oedipus (Cotton-top tamarin).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Platyrrhini;
OC   Callitrichidae; Saguinus.
OX   NCBI_TaxID=9490;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Ceccacci A., Aurisicchio L., Ciliberto G., Palombo F., Traboni C.;
RT   "Recombinant cotton-top tamarin interferon: a new tool for a primate
RT   hepatitis model.";
RL   Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: Secreted protein (By similarity).
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AJ250195; CAC44124.1; -; Genomic_DNA.
DR   HSSP; P01563; 1ITF.
DR   SMR; Q95J78; 24-189.
DR   GO; GO:0005615; C:extracellular space; IEA.
DR   GO; GO:0005126; F:hematopoietin/interferon-class (D200-domain. . .; IEA.
DR   GO; GO:0006952; P:defense response; IEA.
DR   GO; GO:0009615; P:response to virus; IEA.
DR   InterPro; IPR000471; Interferon_abd.
DR   PANTHER; PTHR11691; Interferon_abd; 1.
DR   Pfam; PF00143; Interferon; 1.
DR   PRINTS; PR00266; INTERFERONAB.
DR   ProDom; PD000550; Interferon_abd; 1.
DR   SMART; SM00076; IFabd; 1.
DR   PROSITE; PS00252; INTERFERON_A_B_D; 1.
KW   Antiviral defense; Cytokine; Signal.
FT   SIGNAL        1     23       Potential.
FT   CHAIN        24    189       Potential.
SQ   SEQUENCE   189 AA;  21937 MW;  06A45DD2B631C85C CRC64;

  Query Match             84.8%;  Score 814.5;  DB 2;  Length 189;
  Best Local Similarity   86.2%;  Pred. No. 7.5e-65;
  Matches  163;  Conservative    9;  Mismatches   16;  Indels    1;  Gaps    1;

Qy          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFG 60
              | ||| ||||:||| ||||:||||||||||:||||||||||||| ||||||| ||
Db          1 MTLTFPLLVALVVLSYKSSCSLGCDLPQTHSLGNRRTLMLLAQMRRISPFSCLKDRRDFE 60

Qy         61 FPQEEF-GNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLE 119
              |||||| ||||||  | |||||||| ||||||||||||||||||||| |||||||:||
Db         61 FPQEEFDGNQFQKARAIFVLHEMIQQTFNLFSTKDSSAAWDETLLDKFRTELYQQLNELE 120

Qy        120 ACVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTN 179
              |||:| ||||:|||: ||||| |||||||||||||||||| ||||||||||||||||||
Db        121 ACVVQEVGVTDTPLLNEDSILTVRKYFQRITLYLKEKKYSACAWEVVRAEIMRSFSLSTN 180

Qy        180 LQESLRSKE 188
              ||: ||||:
Db        181 LQKGLRSKK 189


RESULT 5
IFNA5_HUMAN
ID   IFNA5_HUMAN    STANDARD;      PRT;   189 AA.
AC   P01569;
DT   21-JUL-1986, integrated into UniProtKB/Swiss-Prot.
DT   13-AUG-1987, sequence version 1.
DT   07-FEB-2006, entry version 57.
DE   Interferon alpha-5 precursor (Interferon alpha-G) (LeIF G) (Interferon
DE   alpha-61).
GN   Name=IFNA5;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=86037205; PubMed=4057246;
RA   Henco K., Brosius J., Fujisawa A., Fujisawa J., Haynes J.R.,
RA   Hochstadt J., Kovacic T., Pasek M., Schamboeck A., Schmid J.,
RA   Todokoro K., Waelchli M., Nagata S., Weissmann C.;
RT   "Structural relationship of human interferon alpha genes and
RT   pseudogenes.";
RL   J. Mol. Biol. 185:227-260(1985).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX   PubMed=15164053; DOI=10.1038/nature02465;
RA   Humphray S.J., Oliver K., Hunt A.R., Plumb R.W., Loveland J.E.,
RA   Howe K.L., Andrews T.D., Searle S., Hunt S.E., Scott C.E., Jones M.C.,
RA   Ainscough R., Almeida J.P., Ambrose K.D., Ashwell R.I.S.,
RA   Babbage A.K., Babbage S., Bagguley C.L., Bailey J., Banerjee R.,
RA   Barker D.J., Barlow K.F., Bates K., Beasley H., Beasley O., Bird C.P.,
RA   Bray-Allen S., Brown A.J., Brown J.Y., Burford D., Burrill W.,
RA   Burton J., Carder C., Carter N.P., Chapman J.C., Chen Y., Clarke G.,
RA   Clark S.Y., Clee C.M., Clegg S., Collier R.E., Corby N., Crosier M.,
RA   Cummings A.T., Davies J., Dhami P., Dunn M., Dutta I., Dyer L.W.,
RA   Earthrowl M.E., Faulkner L., Fleming C.J., Frankish A.,
RA   Frankland J.A., French L., Fricker D.G., Garner P., Garnett J.,
RA   Ghori J., Gilbert J.G.R., Glison C., Grafham D.V., Gribble S.,
RA   Griffiths C., Griffiths-Jones S., Grocock R., Guy J., Hall R.E.,
RA   Hammond S., Harley J.L., Harrison E.S.I., Hart E.A., Heath P.D.,
RA   Henderson C.D., Hopkins B.L., Howard P.J., Howden P.J., Huckle E.,
RA   Johnson C., Johnson D., Joy A.A., Kay M., Keenan S., Kershaw J.K.,
RA   Kimberley A.M., King A., Knights A., Laird G.K., Langford C.,
RA   Lawlor S., Leongamornlert D.A., Leversha M., Lloyd C., Lloyd D.M.,
RA   Lovell J., Martin S., Mashreghi-Mohammadi M., Matthews L., McLaren S.,
RA   McLay K.E., McMurray A., Milne S., Nickerson T., Nisbett J.,
RA   Nordsiek G., Pearce A.V., Peck A.I., Porter K.M., Pandian R.,
RA   Pelan S., Phillimore B., Povey S., Ramsey Y., Rand V., Scharfe M.,
RA   Sehra H.K., Shownkeen R., Sims S.K., Skuce C.D., Smith M.,
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RA   Steward C.A., Swarbreck D., Sycamore N., Tester J., Thorpe A.,
RA   Tracey A., Tromans A., Thomas D.W., Wall M., Wallis J.M., West A.P.,
RA   Whitehead S.L., Willey D.L., Williams S.A., Wilming L., Wray P.W.,
RA   Young L., Ashurst J.L., Coulson A., Blocker H., Durbin R.,
RA   Sulston J.E., Hubbard T., Jackson M.J., Bentley D.R., Beck S.,
RA   Rogers J., Dunham I.;
RT   "DNA sequence and analysis of human chromosome 9.";
RL   Nature 429:369-374(2004).
RN   [3]
RP   NUCLEOTIDE SEQUENCE OF 57-189.
RC   TISSUE=Spleen;
RX   MEDLINE=81148795; PubMed=6163083;
RA   Goeddel D.V., Leung D.W., Dull T.J., Gross M., Lawn R.M.,
RA   McCandliss R., Seeburg P.H., Ullrich A., Yelverton E., Gray P.W.;
RT   "The structure of eight distinct cloned human leukocyte interferon
RT   cDNAs.";
RL   Nature 290:20-26(1981).
RN   [4]
RP   PROTEIN SEQUENCE OF 22-36.
RX   PubMed=15340161; DOI=10.1110/ps.04682504;
RA   Zhang Z., Henzel W.J.;
RT   "Signal peptide prediction based on analysis of experimentally
RT   verified cleavage sites.";
RL   Protein Sci. 13:2819-2824(2004).
CC   -!- FUNCTION: Produced by macrophages, IFN-alpha have antiviral
CC       activities. Interferon stimulates the production of two enzymes: a
CC       protein kinase and an oligoadenylate synthetase.
CC   -!- SUBCELLULAR LOCATION: Secreted protein.
CC   -!- SIMILARITY: Belongs to the alpha/beta interferon family.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; X02956; CAA26702.1; -; Genomic_DNA.
DR   EMBL; AL162420; CAH73189.1; -; Genomic_DNA.
DR   EMBL; V00541; CAA23802.1; -; mRNA.
DR   PIR; S43716; IVHUA7.
DR   HSSP; P01563; 1ITF.
DR   SMR; P01569; 24-189.
DR   Ensembl; ENSG00000147873; Homo sapiens.
DR   HGNC; HGNC:5426; IFNA5.
DR   MIM; 147565; gene.
DR   LinkHub; P01569; -.
DR   GO; GO:0005126; F:hematopoietin/interferon-class (D200-domain. . .; TAS.
DR   InterPro; IPR000471; Interferon_abd.
DR   PANTHER; PTHR11691; Interferon_abd; 1.
DR   Pfam; PF00143; Interferon; 1.
DR   PRINTS; PR00266; INTERFERONAB.
DR   ProDom; PD000550; Interferon_abd; 1.
DR   SMART; SM00076; IFabd; 1.
DR   PROSITE; PS00252; INTERFERON_A_B_D; 1.
KW   Antiviral defense; Cytokine; Direct protein sequencing; Signal.
FT   SIGNAL        1     21
FT   CHAIN        22    189       Interferon alpha-5.
FT                                 /FTId=PRO_0000016362.
FT   DISULFID     24    122       By similarity.
FT   DISULFID     52    162       By similarity.
SQ   SEQUENCE   189 AA;  21942 MW;  C605992FE2E78043 CRC64;

  Query Match           84.3%;  Score 809.5;  DB 1;  Length 189;
  Best Local Similarity   83.6%;  Pred. No. 2.1e-64;
  Matches  158;  Conservative   11;  Mismatches   19;  Indels    1;  Gaps    1;

Qy          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFG 60
              ||| | ||:||:||:||| ||:||||||||||| :|||||::||| ||| ||||||||||
Db          1 MALPFVLLMALVVLNCKSICSLGCDLPQTHSLSNRRTLMIMAQMGRISPFSCLKDRHDFG 60

Qy         61 FPQEEF-GNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLE 119
              |||||| ||||||| | |||||||| |||||||||| ||||||||||||||||||||
Db         61 FPQEEFDGNQFQKAQAISVLHEMIQQTFNLFSTKDSSATWDETLLDKFYTELYQQLNDLE 120

Qy        120 ACVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTN 179
              ||::| ||| :|||| |||| |||||||||||| |||||||||||||||||||||| |
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Db        121 ACMMQEVGVEDTPLMNVDSILTVRKYFQRITLYLTEKKYSPCAWEVVRAEIMRSFSLSAN 180

Qy        180 LQESLRSKE 188
              ||| || ||
Db        181 LQERLRRKE 189


RESULT 6
Q52LX3_HUMAN
ID   Q52LX3_HUMAN   PRELIMINARY;   PRT;   189 AA.
AC   Q52LX3;
DT   24-MAY-2005, integrated into UniProtKB/TrEMBL.
DT   24-MAY-2005, sequence version 1.
DT   21-FEB-2006, entry version 9.
DE   Interferon, alpha 5.
GN   Name=IFNA5;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Brain;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Brain;
RG   NIH MGC Project;
RL   Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: Secreted protein (By similarity).
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; BC093757; AAH93757.1; -; mRNA.
DR   EMBL; BC093755; AAH93755.1; -; mRNA.
DR   SMR; Q52LX3; 24-189.
DR   Ensembl; ENSG00000147873; Homo sapiens.
DR   GO; GO:0005615; C:extracellular space; IEA.
DR   GO; GO:0005126; F:hematopoietin/interferon-class (D200-domain. . .; IEA.
DR   GO; GO:0006952; P:defense response; IEA.
DR   GO; GO:0009615; P:response to virus; IEA.
DR   InterPro; IPR000471; Interferon_abd.
DR   PANTHER; PTHR11691; Interferon_abd; 1.
DR   Pfam; PF00143; Interferon; 1.
DR   PRINTS; PR00266; INTERFERONAB.
DR   ProDom; PD000550; Interferon_abd; 1.
DR   SMART; SM00076; IFabd; 1.
DR   PROSITE; PS00252; INTERFERON_A_B_D; 1.
KW   Antiviral defense; Cytokine.
SQ   SEQUENCE   189 AA;  21942 MW;  C605992FE2E78043 CRC64;
```

```
  Query Match             84.3%;  Score 809.5;  DB 2;  Length 189;
  Best Local Similarity   83.6%;  Pred. No. 2.1e-64;
  Matches  158;  Conservative   11;  Mismatches   19;  Indels    1;  Gaps    1;

Qy          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFG 60
              ||| | ||:||:||:||| ||:|||||||||| :|||||::||| ||| ||||||||||
Db          1 MALPFVLLMALVVLNCKSICSLGCDLPQTHSLSNRRTLMIMAQMGRISPFSCLKDRHDFG 60

Qy         61 FPQEEF-GNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLE 119
              |||||| ||||||| | |||||||| |||||||||| ||||||||||||||||||||
Db         61 FPQEEFDGNQFQKAQAISVLHEMIQQTFNLFSTKDSSATWDETLLDKFYTELYQQLNDLE 120

Qy        120 ACVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTN 179
              ||::| ||| :|||| |||| |||||||||||| |||||||||||||||||||||| |
Db        121 ACMMQEVGVEDTPLMNVDSILTVRKYFQRITLYLTEKKYSPCAWEVVRAEIMRSFSLSAN 180

Qy        180 LQESLRSKE 188
              ||| || ||
Db        181 LQERLRRKE 189


RESULT 7
IFNA6_HUMAN
ID   IFNA6_HUMAN     STANDARD;      PRT;   189 AA.
AC   P05013;
DT   13-AUG-1987, integrated into UniProtKB/Swiss-Prot.
DT   13-AUG-1987, sequence version 1.
DT   07-FEB-2006, entry version 58.
DE   Interferon alpha-6 precursor (Interferon alpha-K) (LeIF K) (Interferon
DE   alpha-54).
GN   Name=IFNA6;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=86037205; PubMed=4057246;
RA   Henco K., Brosius J., Fujisawa A., Fujisawa J., Haynes J.R.,
RA   Hochstadt J., Kovacic T., Pasek M., Schamboeck A., Schmid J.,
RA   Todokoro K., Waelchli M., Nagata S., Weissmann C.;
RT   "Structural relationship of human interferon alpha genes and
RT   pseudogenes.";
RL   J. Mol. Biol. 185:227-260(1985).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [3]
RP   PROTEIN SEQUENCE OF 21-35.
RX   PubMed=15340161; DOI=10.1110/ps.04682504;
RA   Zhang Z., Henzel W.J.;
RT   "Signal peptide prediction based on analysis of experimentally
RT   verified cleavage sites.";
RL   Protein Sci. 13:2819-2824(2004).
CC   -!- FUNCTION: Produced by macrophages, IFN-alpha have antiviral
CC       activities. Interferon stimulates the production of two enzymes: a
CC       protein kinase and an oligoadenylate synthetase.
CC   -!- SUBCELLULAR LOCATION: Secreted protein.
CC   -!- SIMILARITY: Belongs to the alpha/beta interferon family.
CC   ----------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ----------------------------------------------------------------------
DR   EMBL; X02958; CAA26704.1; -; Genomic_DNA.
DR   EMBL; BC069471; AAH69471.1; -; mRNA.
DR   PIR; A23753; IVHUI6.
DR   HSSP; P01563; 1ITF.
DR   SMR; P05013; 24-189.
DR   Ensembl; ENSG00000120235; Homo sapiens.
DR   HGNC; HGNC:5427; IFNA6.
DR   MIM; 147566; gene.
DR   GO; GO:0005126; F:hematopoietin/interferon-class (D200-domain. . .; NAS.
DR   GO; GO:0009615; P:response to virus; NAS.
DR   InterPro; IPR000471; Interferon_abd.
DR   PANTHER; PTHR11691; Interferon_abd; 1.
DR   Pfam; PF00143; Interferon; 1.
DR   PRINTS; PR00266; INTERFERONAB.
DR   ProDom; PD000550; Interferon_abd; 1.
DR   SMART; SM00076; IFabd; 1.
DR   PROSITE; PS00252; INTERFERON_A_B_D; 1.
KW   Antiviral defense; Cytokine; Direct protein sequencing; Signal.
FT   SIGNAL        1     20
FT   CHAIN        21    189       Interferon alpha-6.
FT                                 /FTId=PRO_0000016363.
FT   DISULFID      24    122       By similarity.
FT   DISULFID      52    162       By similarity.
SQ   SEQUENCE   189 AA;  22141 MW;  8C7F3F90F12C562E CRC64;

  Query Match             84.2%;  Score 808.5;  DB 1;  Length 189;
  Best Local Similarity   85.7%;  Pred. No. 2.6e-64;
  Matches  162;  Conservative    6;  Mismatches   20;  Indels    1;  Gaps    1;

Qy          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFG 60
              ||| ||||:||:|||||||||: |||||||||| |||:||||||||||||||||||||
Db          1 MALPFALLMALVVLSCKSSCSLDCDLPQTHSLGHRRTMMLLAQMRRISLFSCLKDRHDFR 60

Qy         61 FPQEEF-GNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLE 119
              |||||| |||||||| | ||||:||| |||||||||| |||| |||| ||||||||||||
Db         61 FPQEEFDGNQFQKAEAISVLHEVIQQTFNLFSTKDSSVAWDERLLDKLYTELYQQLNDLE 120

Qy        120 ACVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTN 179
              |||:| | |  |||| |||||||||||||||||| |||||||||||||||||||| | |
Db        121 ACVMQEVWVGGTPLMNEDSILAVRKYFQRITLYLTEKKYSPCAWEVVRAEIMRSFSSSRN 180

Qy        180 LQESLRSKE 188
              ||| || ||
Db        181 LQERLRRKE 189


RESULT 8
Q5VYQ1_HUMAN
ID   Q5VYQ1_HUMAN    PRELIMINARY;    PRT;   189 AA.
AC   Q5VYQ1;
DT   10-MAY-2005, integrated into UniProtKB/TrEMBL.
DT   10-MAY-2005, sequence version 1.
DT   21-FEB-2006, entry version 10.
DE   Interferon, alpha 6.
GN   Name=IFNA6; ORFNames=RP11-354P17.7-001;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
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RA   Beasley H.;
RL   Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=PCR rescued clones;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=PCR rescued clones;
RG   NIH MGC Project;
RL   Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=PCR rescued clones;
RG   NIH MGC Project;
RL   Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: Secreted protein (By similarity).
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AL353732; CAH72903.1; -; Genomic_DNA.
DR   EMBL; BC096710; AAH96710.1; -; mRNA.
DR   EMBL; BC096730; AAH96730.1; -; mRNA.
DR   EMBL; BC098357; AAH98357.1; -; mRNA.
DR   EMBL; BC096697; AAH96697.1; -; mRNA.
DR   SMR; Q5VYQ1; 24-189.
DR   Ensembl; ENSG00000120235; Homo sapiens.
DR   GO; GO:0005615; C:extracellular space; IEA.
DR   GO; GO:0005126; F:hematopoietin/interferon-class (D200-domain. . .; IEA.
DR   GO; GO:0006952; P:defense response; IEA.
DR   GO; GO:0009615; P:response to virus; IEA.
DR   InterPro; IPR000471; Interferon_abd.
DR   PANTHER; PTHR11691; Interferon_abd; 1.
DR   Pfam; PF00143; Interferon; 1.
DR   PRINTS; PR00266; INTERFERONAB.
DR   SMART; SM00076; IFabd; 1.
DR   PROSITE; PS00252; INTERFERON_A_B_D; 1.
KW   Antiviral defense; Cytokine.
SQ   SEQUENCE   189 AA;  22141 MW;  8C7F3F90F12C562E CRC64;

  Query Match             84.2%;  Score 808.5;  DB 2;  Length 189;
  Best Local Similarity   85.7%;  Pred. No. 2.6e-64;
  Matches  162;  Conservative    6;  Mismatches   20;  Indels    1;  Gaps    1;

Qy          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFG 60
              ||| |||| :|| :|||||||||: |||||||||| ||| :||||||||||||||||||||
Db          1 MALPFALLMALVVLSCKSSCSLDCDLPQTHSLGHRRTMMLLAQMRRISLFSCLKDRHDFR 60

Qy         61 FPQEEF-GNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLE 119
              |||||| |||||||| | |||| :||| |||||||||| |||| |||| ||||||||||||
Db         61 FPQEEFDGNQFQKAEAISVLHEVIQQTFNLFSTKDSSVAWDERLLDKLYTELYQQLNDLE 120

Qy        120 ACVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTN 179
              |||:| | |  |||| ||||||||||||||||| |||||||||||||||||| | |
Db        121 ACVMQEVWVGGTPLMNEDSILAVRKYFQRITLYLTEKKYSPCAWEVVRAEIMRSFSSSRN 180

Qy        180 LQESLRSKE 188
              ||| || ||
Db        181 LQERLRRKE 189


RESULT 9
IFN14_HUMAN
ID   IFN14_HUMAN    STANDARD;      PRT;   189 AA.
AC   P01570;
DT   21-JUL-1986, integrated into UniProtKB/Swiss-Prot.
DT   21-JUL-1986, sequence version 3.
DT   07-FEB-2006, entry version 63.
DE   Interferon alpha-14 precursor (Interferon alpha-H) (LeIF H)
DE   (Interferon lambda-2-H).
GN   Name=IFNA14;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=86037205; PubMed=4057246;
RA   Henco K., Brosius J., Fujisawa A., Fujisawa J., Haynes J.R.,
RA   Hochstadt J., Kovacic T., Pasek M., Schamboeck A., Schmid J.,
RA   Todokoro K., Waelchli M., Nagata S., Weissmann C.;
RT   "Structural relationship of human interferon alpha genes and
RT   pseudogenes.";
RL   J. Mol. Biol. 185:227-260(1985).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=81201124; PubMed=6165082;
RA   Lawn R.M., Adelman J., Dull T.J., Gross M., Goeddel D.V., Ullrich A.;
RT   "DNA sequence of two closely linked human leukocyte interferon
RT   genes.";
RL   Science 212:1159-1162(1981).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=81148795; PubMed=6163083;
RA   Goeddel D.V., Leung D.W., Dull T.J., Gross M., Lawn R.M.,
RA   McCandliss R., Seeburg P.H., Ullrich A., Yelverton E., Gray P.W.;
RT   "The structure of eight distinct cloned human leukocyte interferon
RT   cDNAs.";
RL   Nature 290:20-26(1981).
RN   [4]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [5]
RP   PROTEIN SEQUENCE OF 24-53, AND CARBOHYDRATE-LINKAGE SITE ASN-95.
```

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RX   MEDLINE=98087498; PubMed=9425112;
RA   Nyman T.A., Toeloe H., Parkkinen J., Kalkkinen N.;
RT   "Identification of nine interferon-alpha subtypes produced by Sendai
RT   virus-induced human peripheral blood leucocytes.";
RL   Biochem. J. 329:295-302(1998).
RN   [6]
RP   ABSENCE OF POLYMORPHISM.
RX   MEDLINE=97067358; PubMed=8910771;
RA   Hussain M., Gill D.S., Liao M.-J.;
RT   "Identification of interferon-alpha 7, -alpha 14, and -alpha 21
RT   variants in the genome of a large human population.";
RL   J. Interferon Cytokine Res. 16:853-859(1996).
CC   -!- FUNCTION: Produced by macrophages, IFN-alpha have antiviral
CC       activities. Interferon stimulates the production of two enzymes: a
CC       protein kinase and an oligoadenylate synthetase.
CC   -!- SUBCELLULAR LOCATION: Secreted protein.
CC   -!- SIMILARITY: Belongs to the alpha/beta interferon family.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; V00533; CAA23794.1; -; Genomic_DNA.
DR   EMBL; X02959; CAA26705.1; -; Genomic_DNA.
DR   EMBL; V00542; CAA23803.1; -; mRNA.
DR   EMBL; BC074956; AAH74956.1; -; mRNA.
DR   PIR; A92916; IVHU14.
DR   HSSP; P01563; 1ITF.
DR   SMR; P01570; 24-189.
DR   GlycoSuiteDB; P01570; -.
DR   HGNC; HGNC:5420; IFNA14.
DR   MIM; 147579; gene.
DR   GO; GO:0005126; F:hematopoietin/interferon-class (D200-domain. . .; TAS.
DR   InterPro; IPR000471; Interferon_abd.
DR   PANTHER; PTHR11691; Interferon_abd; 1.
DR   Pfam; PF00143; Interferon; 1.
DR   PRINTS; PR00266; INTERFERONAB.
DR   ProDom; PD000550; Interferon_abd; 1.
DR   SMART; SM00076; IFabd; 1.
DR   PROSITE; PS00252; INTERFERON_A_B_D; 1.
KW   Antiviral defense; Cytokine; Direct protein sequencing; Glycoprotein;
KW   Signal.
FT   SIGNAL        1     23
FT   CHAIN        24    189       Interferon alpha-14.
FT                                 /FTId=PRO_0000016367.
FT   CARBOHYD     95     95       N-linked (GlcNAc. . .).
FT   DISULFID     24    122       By similarity.
FT   DISULFID     52    162       By similarity.
FT   CONFLICT    175    175       L -> F (in Ref. 3).
SQ   SEQUENCE   189 AA;  22063 MW;  B6B71E2F0D644FE7 CRC64;

  Query Match             82.7%;  Score 793.5;  DB 1;  Length 189;
  Best Local Similarity   82.0%;  Pred. No. 5.8e-63;
  Matches  155;  Conservative   16;  Mismatches   17;  Indels    1;  Gaps    1;

Qy          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFG 60
              ||| |||::||:||||||||||:||:| ||||| :|||||:||||||| ||||||||||
Db          1 MALPFALMMALVVLSCKSSCSLGCNLSQTHSLNNRRTLMLMAQMRRISPFSCLKDRHDFE 60

Qy         61 FPQEEF-GNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLE 119
              |||||| ||||||: | |||||:|| |||||||:||||||||||:||| ||:||:||||
Db         61 FPQEEFDGNQFQKAQAISVLHEMMQQTFNLFSTKNSSAAWDETLLEKFYIELFQQMNDLE 120

Qy        120 ACVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTN 179
              ||||| ||| ||||| |||||||:|||||||||| |||||||||||||||||| | |||
Db        121 ACVIQEVGVEETPLMNEDSILAVKKYFQRITLYLMEKKYSPCAWEVVRAEIMRSLSFSTN 180

Qy        180 LQESLRSKE 188
              ||: || |:
Db        181 LQKRLRRKD 189


RESULT 10
Q5VZ56_HUMAN
ID   Q5VZ56_HUMAN   PRELIMINARY;   PRT;   189 AA.
AC   Q5VZ56;
DT   10-MAY-2005, integrated into UniProtKB/TrEMBL.
DT   10-MAY-2005, sequence version 1.
DT   21-FEB-2006, entry version 9.
DE   Interferon, alpha 14 (IFNA14 protein).
GN   Name=IFNA14; ORFNames=RP11-380P16.9-001;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Beasley H.;
RL   Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=PCR rescued clones;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=PCR rescued clones;
RG   NIH MGC Project;
RL   Submitted (SEP-2005) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: Secreted protein (By similarity).
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AL162420; CAH73187.1; -; Genomic_DNA.
DR   EMBL; BC104159; AAI04160.1; -; mRNA.
DR   EMBL; BC104160; AAI04161.1; -; mRNA.
DR   SMR; Q5VZ56; 24-189.
DR   Ensembl; ENSG00000137026; Homo sapiens.
DR   GO; GO:0005615; C:extracellular space; IEA.
DR   GO; GO:0005126; F:hematopoietin/interferon-class (D200-domain. . .; IEA.
DR   GO; GO:0006952; P:defense response; IEA.
DR   GO; GO:0009615; P:response to virus; IEA.
DR   InterPro; IPR000471; Interferon_abd.
DR   PANTHER; PTHR11691; Interferon_abd; 1.
DR   Pfam; PF00143; Interferon; 1.
DR   PRINTS; PR00266; INTERFERONAB.
DR   SMART; SM00076; IFabd; 1.
DR   PROSITE; PS00252; INTERFERON_A_B_D; 1.
KW   Antiviral defense; Cytokine.
SQ   SEQUENCE   189 AA;  22063 MW;  B6B71E2F0D644FE7 CRC64;

  Query Match             82.7%;  Score 793.5;  DB 2;  Length 189;
  Best Local Similarity   82.0%;  Pred. No. 5.8e-63;
  Matches  155;  Conservative   16;  Mismatches   17;  Indels    1;  Gaps    1;

Qy          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFG 60
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Db          1 MALPFALMMALVVLSCKSSCSLGCNLSQTHSLNNRRTLMLMAQMRRISPFSCLKDRHDFE 60

Qy         61 FPQEEF-GNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLE 119
              |||||| |||||||: | |||||:|| ||||||||:||||||||||:||| ||:||:||||
Db         61 FPQEEFDGNQFQKAQAISVLHEMMQQTFNLFSTKNSSAAWDETLLEKFYIELFQQMNDLE 120

Qy        120 ACVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTN 179
              ||||| ||| ||||| |||||||:|||||||||| |||||||||||||||||| | |||
Db        121 ACVIQEVGVEETPLMNEDSILAVKKYFQRITLYLMEKKYSPCAWEVVRAEIMRSLSFSTN 180

Qy        180 LQESLRSKE 188
                ||: || |:
Db        181 LQKRLRRKD 189


RESULT 11
Q95J77_SAGOE
ID   Q95J77_SAGOE   PRELIMINARY;   PRT;   189 AA.
AC   Q95J77;
DT   01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT   01-DEC-2001, sequence version 1.
DT   21-FEB-2006, entry version 18.
DE   Interferon-alpha precursor.
GN   Name=ifn-alpha;
OS   Saguinus oedipus (Cotton-top tamarin).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Platyrrhini;
OC   Callitrichidae; Saguinus.
OX   NCBI_TaxID=9490;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Ceccacci A., Aurisicchio L., Ciliberto G., Palombo F., Traboni C.;
RT   "Recombinant cotton-top tamarin interferon: a new tool for a primate
RT   hepatitis model.";
RL   Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: Secreted protein (By similarity).
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
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CC   ---------------------------------------------------------------------
DR   EMBL; AJ250196; CAC44125.1; -; Genomic_DNA.
DR   HSSP; P01563; 1ITF.
DR   SMR; Q95J77; 24-189.
DR   GO; GO:0005615; C:extracellular space; IEA.
DR   GO; GO:0005126; F:hematopoietin/interferon-class (D200-domain. . .; IEA.
DR   GO; GO:0006952; P:defense response; IEA.
DR   GO; GO:0009615; P:response to virus; IEA.
DR   InterPro; IPR000471; Interferon_abd.
DR   PANTHER; PTHR11691; Interferon_abd; 1.
DR   Pfam; PF00143; Interferon; 1.
DR   PRINTS; PR00266; INTERFERONAB.
DR   ProDom; PD000550; Interferon_abd; 1.
DR   SMART; SM00076; IFabd; 1.
DR   PROSITE; PS00252; INTERFERON_A_B_D; 1.
KW   Antiviral defense; Cytokine; Signal.
FT   SIGNAL        1     23       Potential.
FT   CHAIN        24    189       interferon-alpha.
SQ   SEQUENCE   189 AA;  22052 MW;  9E4389CFEC329DBA CRC64;

  Query Match             82.2%;  Score 789.5;  DB 2;  Length 189;
  Best Local Similarity   84.1%;  Pred. No. 1.3e-62;
  Matches  159;  Conservative    9;  Mismatches   20;  Indels    1;  Gaps    1;

Qy          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFG 60
              | ||| |||||:||| |||||:||| |||||||:|| |||| |||||| ||||||| ||
Db          1 MTLTFPLLVALVVLSYKSSCSLGCDPPQTHSLGNRRNLMLLVQMRRISPFSCLKDRRDFE 60

Qy         61 FPQEEF-GNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLE 119
              ||||||  ||||||  | |||||||| |||||||||||||||||||| |||||||:||
Db         61 FPQEEFDDNQFQKARAIFVLHEMIQQTFNLFSTKDSSAAWDETLLDKFRTELYQQLNELE 120

Qy        120 ACVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTN 179
              |||||| ||| ||||| |||||||:|||||||||| |||||||||||||||||| | |||
Db        121 ACVMQEVGVTDTPLLNEDSILTVRKYFQRITLYLKEKKYSACAWEVVRAEIMRSFSLSTN 180

Qy        180 LQESLRSKE 188
                ||: ||||:
Db        181 LQKGLRSKK 189


RESULT 12
Q6QNB6_HUMAN
ID   Q6QNB6_HUMAN   PRELIMINARY;   PRT;   154 AA.
AC   Q6QNB6;
DT   05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT   05-JUL-2004, sequence version 1.
DT   07-FEB-2006, entry version 11.
DE   Interferon alpha A (Fragment).
GN   Name=IFNA;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Behravan J., Ahmadpour H.;
RL   Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AY532915; AAS92248.1; -; Genomic_DNA.
DR   HSSP; P56828; 1B5L.
DR   SMR; Q6QNB6; 1-154.
DR   Ensembl; ENSG00000188379; Homo sapiens.
DR   GO; GO:0005615; C:extracellular space; IEA.
DR   GO; GO:0005126; F:hematopoietin/interferon-class (D200-domain. . .; IEA.
DR   GO; GO:0006952; P:defense response; IEA.
DR   GO; GO:0009615; P:response to virus; IEA.
DR   InterPro; IPR000471; Interferon_abd.
DR   PANTHER; PTHR11691; Interferon_abd; 1.
DR   Pfam; PF00143; Interferon; 1.
DR   PRINTS; PR00266; INTERFERONAB.
DR   ProDom; PD000550; Interferon_abd; 1.
DR   SMART; SM00076; IFabd; 1.
DR   PROSITE; PS00252; INTERFERON_A_B_D; 1.
KW   Antiviral defense; Cytokine.
FT   NON_TER       1      1
FT   NON_TER     154    154
SQ   SEQUENCE   154 AA;  17963 MW;  013C1BB58B7EE4A3 CRC64;

  Query Match             81.9%;  Score 786;  DB 2;  Length 154;
  Best Local Similarity   98.7%;  Pred. No. 2.1e-62;
  Matches  152;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         25 DLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFGFPQEEFGNQFQKAETIPVLHEMIQ 84
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 DLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFGFPQEEFGNQFQKAETIPVLHEMIQ 60

Qy         85 QIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEACVIQGVGVTETPLMKEDSILAVRK 144
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 QIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEACVIQGVGVTETPLMKEDSILAVRK 120

Qy        145 YFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLST 178
              |||||||||||||||||| |||||||||| |
Db        121 YFQRITLYLKEKKYSPCAWEAVRAEIMRSFSLPT 154


RESULT 13
IFNA4_HUMAN
ID   IFNA4_HUMAN    STANDARD;      PRT;   189 AA.
AC   P05014; P13358;
DT   13-AUG-1987, integrated into UniProtKB/Swiss-Prot.
DT   10-MAY-2005, sequence version 2.
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DT   07-FEB-2006, entry version 61.
DE   Interferon alpha-4 precursor (Interferon alpha-4B) (Interferon alpha-
DE   M1) (Interferon alpha-76).
GN   Name=IFNA4;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE, AND VARIANTS ALPHA-4B THR-74 AND VAL-137.
RX   MEDLINE=86037205; PubMed=4057246;
RA   Henco K., Brosius J., Fujisawa A., Fujisawa J., Haynes J.R.,
RA   Hochstadt J., Kovacic T., Pasek M., Schamboeck A., Schmid J.,
RA   Todokoro K., Waelchli M., Nagata S., Weissmann C.;
RT   "Structural relationship of human interferon alpha genes and
RT   pseudogenes.";
RL   J. Mol. Biol. 185:227-260(1985).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=84307815; PubMed=6089830;
RA   Linnane A.W., Beilharz M.W., McMullen G.L., Macreadie I.G., Murphy M.,
RA   Nisbet I.T., Novitski C.E., Woodrow G.C.;
RT   "Nucleotide sequence and expression in E. coli of a human interferon-
RT   alpha gene selected from a genomic library using synthetic
RT   oligonucleotides.";
RL   Biochem. Int. 8:725-732(1984).
RN   [3]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA], AND VARIANT THR-74.
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [4]
RP   PROTEIN SEQUENCE OF 24-56.
RX   MEDLINE=98087498; PubMed=9425112;
RA   Nyman T.A., Toeloe H., Parkkinen J., Kalkkinen N.;
RT   "Identification of nine interferon-alpha subtypes produced by Sendai
RT   virus-induced human peripheral blood leucocytes.";
RL   Biochem. J. 329:295-302(1998).
RN   [5]
RP   POLYMORPHISM.
RX   MEDLINE=97474410; PubMed=9335434;
RA   Hussain M., Gill D.S., Liao M.-J.;
RT   "Both variant forms of interferon-alpha4 gene (IFNA4a and IFNA4b) are
RT   present in the human population.";
RL   J. Interferon Cytokine Res. 17:559-566(1997).
CC   -!- FUNCTION: Produced by macrophages, IFN-alpha have antiviral
CC       activities. Interferon stimulates the production of two enzymes: a
CC       protein kinase and an oligoadenylate synthetase.
CC   -!- SUBCELLULAR LOCATION: Secreted protein.
CC   -!- POLYMORPHISM: Two forms exist; alpha-4a (shown here) and alpha-4b.
CC       They seem to be equally abundant.
CC   -!- SIMILARITY: Belongs to the alpha/beta interferon family.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; X02955; CAA26701.1; -; Genomic_DNA.
DR   EMBL; M27318; AAA52726.1; -; mRNA.
DR   EMBL; BC074965; AAH74965.1; -; mRNA.
DR   EMBL; BC074966; AAH74966.1; -; mRNA.
DR   PIR; E23753; IVHU4B.
DR   PIR; I52347; I52347.
DR   HSSP; P01563; 1ITF.
DR   SMR; P05014; 24-189.
DR   Ensembl; ENSG00000147877; Homo sapiens.
DR   HGNC; HGNC:5425; IFNA4.
DR   MIM; 147564; gene.
DR   GO; GO:0005132; F:interferon-alpha/beta receptor binding; TAS.
DR   GO; GO:0009615; P:response to virus; TAS.
DR   InterPro; IPR000471; Interferon_abd.
DR   PANTHER; PTHR11691; Interferon_abd; 1.
DR   Pfam; PF00143; Interferon; 1.
DR   PRINTS; PR00266; INTERFERONAB.
DR   SMART; SM00076; IFabd; 1.
DR   PROSITE; PS00252; INTERFERON_A_B_D; 1.
KW   Antiviral defense; Cytokine; Direct protein sequencing; Polymorphism;
KW   Signal.
FT   SIGNAL        1     23
FT   CHAIN        24    189       Interferon alpha-4.
FT                                 /FTId=PRO_0000016361.
FT   DISULFID     24    122       By similarity.
FT   DISULFID     52    162       By similarity.
FT   VARIANT      74     74       A -> T (in alpha-4B; dbSNP:1062571).
FT                                 /FTId=VAR_013002.
FT   VARIANT     137    137       E -> V (in alpha-4B; dbSNP:3750480).
FT                                 /FTId=VAR_013003.
SQ   SEQUENCE   189 AA;  21808 MW;  828DF9C33ABC337F CRC64;

  Query Match             81.4%;  Score 781.5;  DB 1;  Length 189;
  Best Local Similarity   81.5%;  Pred. No. 6.9e-62;
  Matches  154;  Conservative   17;  Mismatches   17;  Indels    1;  Gaps    1;

Qy          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFG 60
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Db          1 MALSFSLLMAVLVLSYKSICSLGCDLPQTHSLGNRRALILLAQMGRISHFSCLKDRHDFG 60

Qy         61 FPQEEF-GNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLE 119
              ||:||| |:|||||: | |||||||| |||||||:|||||:::||:|| ||||||||||
Db         61 FPEEEFDGHQFQKAQAISVLHEMIQQTFNLFSTEDSSAAWEQSLLEKFSTELYQQLNDLE 120

Qy        120 ACVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTN 179
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Qy        180 LQESLRSKE 188
                ||: || |:
Db        181 LQKRLRRKD 189


RESULT 14
Q5VV15_HUMAN
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AC   Q5VV15;
DT   07-DEC-2004, integrated into UniProtKB/TrEMBL.
DT   07-DEC-2004, sequence version 1.
DT   21-FEB-2006, entry version 10.
DE   Interferon, alpha 4.
GN   Name=IFNA4; ORFNames=RP11-1P8.4-001;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Pelan S.;
RL   Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
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CC   -!- SUBCELLULAR LOCATION: Secreted protein (By similarity).
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AL512606; CAH71188.1; -; Genomic_DNA.
DR   SMR; Q5VV15; 24-189.
DR   Ensembl; ENSG00000147877; Homo sapiens.
DR   LinkHub; Q5VV15; -.
DR   GO; GO:0005615; C:extracellular space; IEA.
DR   GO; GO:0005126; F:hematopoietin/interferon-class (D200-domain. . .; IEA.
DR   GO; GO:0006952; P:defense response; IEA.
DR   GO; GO:0009615; P:response to virus; IEA.
DR   InterPro; IPR000471; Interferon_abd.
DR   PANTHER; PTHR11691; Interferon_abd; 1.
DR   Pfam; PF00143; Interferon; 1.
DR   PRINTS; PR00266; INTERFERONAB.
DR   ProDom; PD000550; Interferon_abd; 1.
DR   SMART; SM00076; IFabd; 1.
DR   PROSITE; PS00252; INTERFERON_A_B_D; 1.
KW   Antiviral defense; Cytokine.
SQ   SEQUENCE   189 AA;  21808 MW;  828DF9C33ABC337F CRC64;

  Query Match             81.4%;  Score 781.5;  DB 2;  Length 189;
  Best Local Similarity   81.5%;  Pred. No. 6.9e-62;
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Qy          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFG 60
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Db         61 FPEEEFDGHQFQKAQAISVLHEMIQQTFNLFSTEDSSAAWEQSLLEKFSTELYQQLNDLE 120

Qy        120 ACVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTN 179
              ||||| ||| ||||| |||||||||||||||||| |||||||||||||||||| | |||
Db        121 ACVIQEVGVEETPLMNEDSILAVRKYFQRITLYLTEKKYSPCAWEVVRAEIMRSLSFSTN 180

Qy        180 LQESLRSKE 188
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RESULT 15
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ID   Q52LB8_HUMAN   PRELIMINARY;   PRT;   189 AA.
AC   Q52LB8;
DT   24-MAY-2005, integrated into UniProtKB/TrEMBL.
DT   24-MAY-2005, sequence version 1.
DT   21-FEB-2006, entry version 10.
DE   Interferon, alpha 13.
GN   Name=IFNA13;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Brain;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Brain;
RG   NIH MGC Project;
RL   Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Brain;
RG   NIH MGC Project;
RL   Submitted (JAN-2006) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: Secreted protein (By similarity).
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; BC093988; AAH93988.1; -; mRNA.
DR   EMBL; BC112002; AAI12003.1; -; mRNA.
DR   SMR; Q52LB8; 24-189.
DR   Ensembl; ENSG00000120247; Homo sapiens.
DR   GO; GO:0005615; C:extracellular space; IEA.
DR   GO; GO:0005126; F:hematopoietin/interferon-class (D200-domain. . .; IEA.
DR   GO; GO:0006952; P:defense response; IEA.
DR   GO; GO:0009615; P:response to virus; IEA.
DR   InterPro; IPR000471; Interferon_abd.
DR   PANTHER; PTHR11691; Interferon_abd; 1.
DR   Pfam; PF00143; Interferon; 1.
DR   PRINTS; PR00266; INTERFERONAB.
DR   ProDom; PD000550; Interferon_abd; 1.
DR   SMART; SM00076; IFabd; 1.
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KW   Antiviral defense; Cytokine.
SQ   SEQUENCE   189 AA;  21697 MW;  442F8BB754D88398 CRC64;

  Query Match             80.9%;  Score 776.5;  DB 2;  Length 189;
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Qy         61 FPQEEF-GNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLE 119
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Qy        120 ACVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTN 179
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Db        121 ACVMQEERVGETPLMNADSILAVKKYFRRITLYLTEKKYSPCAWEVVRAEIMRSLSLSTN 180

Qy        180 LQESLRSKE 188
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Db        181 LQERLRRKE 189


Search completed: October 14, 2006, 08:01:49
Job time : 303 secs
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OM protein - protein search, using sw model

Run on: October 14, 2006, 08:02:07 ; Search time 53 Seconds
(without alignments)
310.486 Million cell updates/sec

Title: US-10-653-350-1
Perfect score: 960
Sequence: 1 MALTFALLVALLVLSCKSSC.....EIMRSFSLSTNLQESLRSKE 188

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
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7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	960	100.0	188	2	US-07-145-002B-26	Sequence 26, Appl
2	960	100.0	188	2	US-07-145-002B-35	Sequence 35, Appl
3	960	100.0	188	2	US-06-256-204C-26	Sequence 26, Appl
4	960	100.0	188	2	US-06-256-204C-35	Sequence 35, Appl
5	960	100.0	188	2	US-09-949-016-5966	Sequence 5966, Ap
6	960	100.0	188	2	US-09-915-873A-4	Sequence 4, Appli
7	960	100.0	205	2	US-09-949-016-8552	Sequence 8552, Ap
8	957	99.7	188	2	US-09-206-903A-7	Sequence 7, Appli
9	957	99.7	188	2	US-09-202-122-7	Sequence 7, Appli
10	957	99.7	188	2	US-09-206-935-9	Sequence 9, Appli
11	957	99.7	188	2	US-07-145-002B-2	Sequence 2, Appli
12	957	99.7	188	2	US-07-145-002B-17	Sequence 17, Appl
13	957	99.7	188	2	US-09-919-622A-7	Sequence 7, Appli
14	957	99.7	188	2	US-06-256-204C-2	Sequence 2, Appli
15	957	99.7	188	2	US-06-256-204C-17	Sequence 17, Appl
16	957	99.7	188	2	US-09-962-625-1	Sequence 1, Appli
17	957	99.7	188	2	US-09-599-413-3	Sequence 3, Appli
18	943	98.2	188	2	US-09-206-936-9	Sequence 9, Appli
19	937.5	97.7	189	1	US-08-026-758-4	Sequence 4, Appli
20	937	97.6	219	7	5310729-4	Patent No. 5310729
21	934.5	97.3	189	1	US-08-026-758-5	Sequence 5, Appli
22	929.5	96.8	189	7	5510472-7	Patent No. 5510472
23	895	93.2	195	7	5198345-17	Patent No. 5198345
24	851.5	88.7	188	1	US-08-249-671A-11	Sequence 11, Appl
25	851	88.6	165	1	US-08-024-330-1	Sequence 1, Appli
26	851	88.6	165	1	US-07-952-840-1	Sequence 1, Appli
27	851	88.6	165	1	US-08-356-021-1	Sequence 1, Appli
28	851	88.6	165	2	US-09-462-941-3	Sequence 3, Appli
29	851	88.6	165	2	US-06-256-204C-79	Sequence 79, Appl
30	851	88.6	165	2	US-09-915-873A-5	Sequence 5, Appli
31	851	88.6	165	5	PCT-US94-01729-1	Sequence 1, Appli
32	851	88.6	166	2	US-07-145-002B-53	Sequence 53, Appl
33	851	88.6	166	2	US-06-256-204C-53	Sequence 53, Appl
34	851	88.6	198	2	US-09-333-348B-11	Sequence 11, Appl
35	848	88.3	165	2	US-06-256-204C-71	Sequence 71, Appl
36	848	88.3	166	2	US-07-145-002B-45	Sequence 45, Appl
37	848	88.3	166	2	US-06-256-204C-45	Sequence 45, Appl
38	848	88.3	181	2	US-09-723-942-18	Sequence 18, Appl
39	848	88.3	181	2	US-09-723-775-18	Sequence 18, Appl
40	845	88.0	165	2	US-09-216-500-1	Sequence 1, Appli
41	845	88.0	165	2	US-09-730-464-1	Sequence 1, Appli
42	843	87.8	165	1	US-08-249-671A-5	Sequence 5, Appli
43	840.5	87.6	166	2	US-08-819-238A-1	Sequence 1, Appli
44	840.5	87.6	166	2	US-09-379-434-1	Sequence 1, Appli
45	835	87.0	165	7	5210029-3	Patent No. 5210029

ALIGNMENTS

RESULT 1
US-07-145-002B-26
; Sequence 26, Application US/07145002B
; Patent No. 6482613
; GENERAL INFORMATION:
; APPLICANT: Goeddel, David V.
; APPLICANT: Pestka, Sidney
; TITLE OF INVENTION: MICROBIAL PRODUCTION OF MATURE HUMAN
; TITLE OF INVENTION: LEUKOCYTE INTERFERONS
; FILE REFERENCE: 1803-0088-999
; CURRENT APPLICATION NUMBER: US/07/145,002B
; CURRENT FILING DATE: 1989-01-19
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Homo sapiens
US-07-145-002B-26

Query Match 100.0%; Score 960; DB 2; Length 188;
Best Local Similarity 100.0%; Pred. No. 1.5e-103;
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFG 60
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Db          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFG 60

Qy         61 FPQEEFGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEA 120
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Db         61 FPQEEFGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEA 120

Qy        121 CVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNL 180
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Db        121 CVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNL 180

Qy        181 QESLRSKE 188
              ||||||||
Db        181 QESLRSKE 188
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RESULT 2
US-07-145-002B-35
; Sequence 35, Application US/07145002B
; Patent No. 6482613
; GENERAL INFORMATION:
; APPLICANT: Goeddel, David V.
; APPLICANT: Pestka, Sidney
; TITLE OF INVENTION: MICROBIAL PRODUCTION OF MATURE HUMAN

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;  TITLE OF INVENTION:  LEUKOCYTE INTERFERONS
;  FILE REFERENCE: 1803-0088-999
;  CURRENT APPLICATION NUMBER: US/07/145,002B
;  CURRENT FILING DATE:  1989-01-19
;  NUMBER OF SEQ ID NOS: 70
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 35
;   LENGTH: 188
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-07-145-002B-35

  Query Match             100.0%;  Score 960;  DB 2;  Length 188;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-103;
  Matches  188;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy        181 QESLRSKE 188
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Db        181 QESLRSKE 188


RESULT 3
US-06-256-204C-26
; Sequence 26, Application US/06256204C
; Patent No. 6610830
; GENERAL INFORMATION:
;  APPLICANT: Goeddel, David V.
;  APPLICANT:  Pestka, Sidney
;  TITLE OF INVENTION: MICROBIAL PRODUCTION OF MATURE HUMAN
;  TITLE OF INVENTION:  LEUKOCYTE INTERFERONS
;  FILE REFERENCE: 1803-0025-999
;  CURRENT APPLICATION NUMBER: US/06/256,204C
;  CURRENT FILING DATE:  1981-04-21
;  NUMBER OF SEQ ID NOS: 85
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 26
;   LENGTH: 188
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-06-256-204C-26

  Query Match             100.0%;  Score 960;  DB 2;  Length 188;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-103;
  Matches  188;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy        121 CVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNL 180

Qy        181 QESLRSKE 188
              ||||||||
Db        181 QESLRSKE 188


RESULT 4
US-06-256-204C-35
; Sequence 35, Application US/06256204C
; Patent No. 6610830
; GENERAL INFORMATION:
;  APPLICANT: Goeddel, David V.
;  APPLICANT:  Pestka, Sidney
;  TITLE OF INVENTION: MICROBIAL PRODUCTION OF MATURE HUMAN
;  TITLE OF INVENTION:  LEUKOCYTE INTERFERONS
;  FILE REFERENCE: 1803-0025-999
;  CURRENT APPLICATION NUMBER: US/06/256,204C
;  CURRENT FILING DATE:  1981-04-21
;  NUMBER OF SEQ ID NOS: 85
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 35
;   LENGTH: 188
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-06-256-204C-35

  Query Match             100.0%;  Score 960;  DB 2;  Length 188;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-103;
  Matches  188;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFG 60

Qy         61 FPQEEFGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FPQEEFGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEA 120

Qy        121 CVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNL 180

Qy        181 QESLRSKE 188
              ||||||||
Db        181 QESLRSKE 188


RESULT 5
US-09-949-016-5966
; Sequence 5966, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5966
;   LENGTH: 188
;   TYPE: PRT
;   ORGANISM: Human
US-09-949-016-5966

  Query Match             100.0%;  Score 960;  DB 2;  Length 188;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-103;
  Matches  188;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFG 60

Qy         61 FPQEEFGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FPQEEFGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEA 120

Qy        121 CVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNL 180

Qy        181 QESLRSKE 188
              ||||||||
Db        181 QESLRSKE 188
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RESULT 6
US-09-915-873A-4
; Sequence 4, Application US/09915873A
; Patent No. 6815184
; GENERAL INFORMATION:
; APPLICANT: Stomp, Anne-Marie
; APPLICANT: Dickey, Lynn
; APPLICANT: Gasdaska, John
; TITLE OF INVENTION: Expression of Biologically Active
; TITLE OF INVENTION: Polypeptides in Duckweed
; FILE REFERENCE: 40989/237225
; CURRENT APPLICATION NUMBER: US/09/915,873A
; CURRENT FILING DATE: 2001-07-26
; PRIOR APPLICATION NUMBER: US 60/293,330
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/221,705
; PRIOR FILING DATE: 2000-07-31
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-915-873A-4

Query Match 100.0%; Score 960; DB 2; Length 188;
Best Local Similarity 100.0%; Pred. No. 1.5e-103;
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFG 60

Qy         61 FPQEEFGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FPQEEFGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEA 120

Qy        121 CVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNL 180

Qy        181 QESLRSKE 188
              ||||||||
Db        181 QESLRSKE 188
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RESULT 7
US-09-949-016-8552
; Sequence 8552, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8552
; LENGTH: 205
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8552

Query Match 100.0%; Score 960; DB 2; Length 205;
Best Local Similarity 100.0%; Pred. No. 1.7e-103;
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         18 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFG 77

Qy         61 FPQEEFGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         78 FPQEEFGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEA 137

Qy        121 CVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        138 CVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNL 197

Qy        181 QESLRSKE 188
              ||||||||
Db        198 QESLRSKE 205
```

RESULT 8
US-09-206-903A-7
; Sequence 7, Application US/09206903A
; Patent No. 6200780
; GENERAL INFORMATION:
; APPLICANT: Chen, Jian
; APPLICANT: Godowski, Paul J.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Dong-Xiao
; TITLE OF INVENTION: NOVEL TYPE I INTERFERONS
; FILE REFERENCE: P1224-2R1
; CURRENT APPLICATION NUMBER: US/09/206,903A
; CURRENT FILING DATE: 1998-12-07
; PRIOR APPLICATION NUMBER: US 60/106,463
; PRIOR FILING DATE: 1998-10-30
; NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 7
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-206-903A-7

Query Match 99.7%; Score 957; DB 2; Length 188;
Best Local Similarity 99.5%; Pred. No. 3.3e-103;
Matches 187; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFG 60
              |||||||||||||||||||||||||||||||||||||||||||:||||||||||||||||
Db          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRKISLFSCLKDRHDFG 60

Qy         61 FPQEEFGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FPQEEFGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEA 120

Qy        121 CVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNL 180

Qy        181 QESLRSKE 188
```

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                ||||||||
Db        181 QESLRSKE 188


RESULT 9
US-09-202-122-7
; Sequence 7, Application US/09202122
; Patent No. 6299869
; GENERAL INFORMATION:
;  APPLICANT:  Chen, Jian
;  APPLICANT:  Godowski, Paul
;  APPLICANT:  Wood, William I.
;  APPLICANT:  Zhang, Dong-Xiao
;  TITLE OF INVENTION:  HUMAN INTERFERON-EPSILON: A TYPE I INTERFERON
;  FILE REFERENCE:  P1224R2 (filed)
;  CURRENT APPLICATION NUMBER: US/09/202,122
;  CURRENT FILING DATE:  1999-03-04
;  PRIOR APPLICATION NUMBER:  PCT/US98/25672
;  PRIOR FILING DATE:  1998-12-03
;  NUMBER OF SEQ ID NOS:  12
; SEQ ID NO 7
;   LENGTH: 188
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-202-122-7

  Query Match             99.7%;  Score 957;  DB 2;  Length 188;
  Best Local Similarity   99.5%;  Pred. No. 3.3e-103;
  Matches  187;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFG 60
              |||||||||||||||||||||||||||||||||||||||||||:|||||||||||||||
Db          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRKISLFSCLKDRHDFG 60

Qy         61 FPQEEFGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FPQEEFGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEA 120

Qy        121 CVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNL 180

Qy        181 QESLRSKE 188
              ||||||||
Db        181 QESLRSKE 188


RESULT 10
US-09-206-935-9
; Sequence 9, Application US/09206935
; Patent No. 6299877
; GENERAL INFORMATION:
;  APPLICANT: Chen, Jian
;  APPLICANT: Godowski, Paul
;  APPLICANT: Wood, William I.
;  APPLICANT: Zhang, Dong-Xiao
;  TITLE OF INVENTION: NOVEL TYPE I INTERFERONS
;  FILE REFERENCE: 11669.50US05
;  CURRENT APPLICATION NUMBER: US/09/206,935
;  CURRENT FILING DATE: 1998-12-07
;  EARLIER APPLICATION NUMBER: 60/084,045
;  EARLIER FILING DATE: 1998-05-04
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
;   LENGTH: 188
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-206-935-9

  Query Match             99.7%;  Score 957;  DB 2;  Length 188;
  Best Local Similarity   99.5%;  Pred. No. 3.3e-103;
  Matches  187;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFG 60
              |||||||||||||||||||||||||||||||||||||||||||:|||||||||||||||
Db          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRKISLFSCLKDRHDFG 60

Qy         61 FPQEEFGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FPQEEFGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEA 120

Qy        121 CVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNL 180

Qy        181 QESLRSKE 188
              ||||||||
Db        181 QESLRSKE 188


RESULT 11
US-07-145-002B-2
; Sequence 2, Application US/07145002B
; Patent No. 6482613
; GENERAL INFORMATION:
;  APPLICANT: Goeddel, David V.
;  APPLICANT:  Pestka, Sidney
;  TITLE OF INVENTION: MICROBIAL PRODUCTION OF MATURE HUMAN
;  TITLE OF INVENTION:  LEUKOCYTE INTERFERONS
;  FILE REFERENCE: 1803-0088-999
;  CURRENT APPLICATION NUMBER: US/07/145,002B
;  CURRENT FILING DATE:  1989-01-19
;  NUMBER OF SEQ ID NOS: 70
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
;   LENGTH: 188
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-07-145-002B-2

  Query Match             99.7%;  Score 957;  DB 2;  Length 188;
  Best Local Similarity   99.5%;  Pred. No. 3.3e-103;
  Matches  187;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFG 60
              |||||||||||||||||||||||||||||||||||||||||||:|||||||||||||||
Db          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRKISLFSCLKDRHDFG 60

Qy         61 FPQEEFGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FPQEEFGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEA 120

Qy        121 CVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNL 180

Qy        181 QESLRSKE 188
              ||||||||
Db        181 QESLRSKE 188


RESULT 12
US-07-145-002B-17
; Sequence 17, Application US/07145002B
; Patent No. 6482613
; GENERAL INFORMATION:
;  APPLICANT: Goeddel, David V.
;  APPLICANT:  Pestka, Sidney
;  TITLE OF INVENTION: MICROBIAL PRODUCTION OF MATURE HUMAN
;  TITLE OF INVENTION:  LEUKOCYTE INTERFERONS
;  FILE REFERENCE: 1803-0088-999
;  CURRENT APPLICATION NUMBER: US/07/145,002B
;  CURRENT FILING DATE:  1989-01-19
;  NUMBER OF SEQ ID NOS: 70
;  SOFTWARE: FastSEQ for Windows Version 3.0
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; SEQ ID NO 17
;   LENGTH: 188
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-07-145-002B-17

  Query Match             99.7%;  Score 957;  DB 2;  Length 188;
  Best Local Similarity   99.5%;  Pred. No. 3.3e-103;
  Matches  187;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFG 60
              |||||||||||||||||||||||||||||||||||||||||||:|||||||||||||||
Db          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRKISLFSCLKDRHDFG 60

Qy         61 FPQEEFGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FPQEEFGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEA 120

Qy        121 CVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNL 180

Qy        181 QESLRSKE 188
              ||||||||
Db        181 QESLRSKE 188


RESULT 13
US-09-919-622A-7
; Sequence 7, Application US/09919622A
; Patent No. 6569420
; GENERAL INFORMATION:
;  APPLICANT: Chen, Jian
;  APPLICANT:  Godowski, Paul
;  APPLICANT:  Wood, William I.
;  APPLICANT:  Zhang, Dong-Xiao
;  TITLE OF INVENTION: HUMAN INTERFERON-EPSILON: A TYPE I INTERFERON
;  FILE REFERENCE: P1224R2C1 (replacement)
;  CURRENT APPLICATION NUMBER: US/09/919,622A
;  CURRENT FILING DATE:  2001-07-30
;  PRIOR APPLICATION NUMBER: US 09/202122,
;  PRIOR FILING DATE: 1999-03-04
;  PRIOR APPLICATION NUMBER: PCT/US98/25672
;  PRIOR FILING DATE: 1998-12-03
;  NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 7
;   LENGTH: 188
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-919-622A-7

  Query Match             99.7%;  Score 957;  DB 2;  Length 188;
  Best Local Similarity   99.5%;  Pred. No. 3.3e-103;
  Matches  187;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFG 60
              |||||||||||||||||||||||||||||||||||||||||||:|||||||||||||||
Db          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRKISLFSCLKDRHDFG 60

Qy         61 FPQEEFGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FPQEEFGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEA 120

Qy        121 CVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNL 180

Qy        181 QESLRSKE 188
              ||||||||
Db        181 QESLRSKE 188


RESULT 14
US-06-256-204C-2
; Sequence 2, Application US/06256204C
; Patent No. 6610830
; GENERAL INFORMATION:
;  APPLICANT: Goeddel, David V.
;  APPLICANT:  Pestka, Sidney
;  TITLE OF INVENTION: MICROBIAL PRODUCTION OF MATURE HUMAN
;  TITLE OF INVENTION:  LEUKOCYTE INTERFERONS
;  FILE REFERENCE: 1803-0025-999
;  CURRENT APPLICATION NUMBER: US/06/256,204C
;  CURRENT FILING DATE:  1981-04-21
;  NUMBER OF SEQ ID NOS: 85
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
;   LENGTH: 188
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-06-256-204C-2

  Query Match             99.7%;  Score 957;  DB 2;  Length 188;
  Best Local Similarity   99.5%;  Pred. No. 3.3e-103;
  Matches  187;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFG 60
              |||||||||||||||||||||||||||||||||||||||||||:|||||||||||||||
Db          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRKISLFSCLKDRHDFG 60

Qy         61 FPQEEFGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FPQEEFGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEA 120

Qy        121 CVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNL 180

Qy        181 QESLRSKE 188
              ||||||||
Db        181 QESLRSKE 188


RESULT 15
US-06-256-204C-17
; Sequence 17, Application US/06256204C
; Patent No. 6610830
; GENERAL INFORMATION:
;  APPLICANT: Goeddel, David V.
;  APPLICANT:  Pestka, Sidney
;  TITLE OF INVENTION: MICROBIAL PRODUCTION OF MATURE HUMAN
;  TITLE OF INVENTION:  LEUKOCYTE INTERFERONS
;  FILE REFERENCE: 1803-0025-999
;  CURRENT APPLICATION NUMBER: US/06/256,204C
;  CURRENT FILING DATE:  1981-04-21
;  NUMBER OF SEQ ID NOS: 85
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 17
;   LENGTH: 188
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-06-256-204C-17

  Query Match             99.7%;  Score 957;  DB 2;  Length 188;
  Best Local Similarity   99.5%;  Pred. No. 3.3e-103;
  Matches  187;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

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Db          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRKISLFSCLKDRHDFG 60

Qy         61 FPQEEFGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEA 120
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Db         61 FPQEEFGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEA 120

Qy        121 CVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNL 180
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Db        121 CVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNL 180

Qy        181 QESLRSKE 188
              ||||||||
Db        181 QESLRSKE 188
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Search completed: October 14, 2006, 08:03:34
Job time : 54 secs

GenCore version 5.1.9

OM protein - protein search, using sw model

Run on: October 14, 2006, 08:02:52 ; Search time 179 Seconds
(without alignments)
486.505 Million cell updates/sec

Title: US-10-653-350-1
Perfect score: 960
Sequence: 1 MALTFALLVALLVLSCKSSC.....EIMRSFSLSTNLQESLRSKE 188

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_Main:*
1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	960	100.0	188	3	US-09-881-050-24	Sequence 24, Appl
2	960	100.0	188	3	US-09-915-873-4	Sequence 4, Appli
3	960	100.0	188	4	US-10-087-325-2	Sequence 2, Appli
4	960	100.0	188	4	US-10-411-037-4	Sequence 4, Appli
5	960	100.0	188	4	US-10-411-026-4	Sequence 4, Appli
6	960	100.0	188	4	US-10-410-962-4	Sequence 4, Appli
7	960	100.0	188	4	US-10-411-049-4	Sequence 4, Appli
8	960	100.0	188	4	US-10-410-930-4	Sequence 4, Appli
9	960	100.0	188	4	US-10-410-997-4	Sequence 4, Appli
10	960	100.0	188	4	US-10-411-012-4	Sequence 4, Appli
11	960	100.0	188	4	US-10-287-994-4	Sequence 4, Appli
12	960	100.0	188	4	US-10-410-913-4	Sequence 4, Appli
13	960	100.0	188	5	US-10-276-642-12	Sequence 12, Appl
14	960	100.0	188	5	US-10-794-615-4	Sequence 4, Appli
15	960	100.0	188	5	US-10-653-350-1	Sequence 1, Appli
16	960	100.0	188	5	US-10-410-980-4	Sequence 4, Appli
17	960	100.0	188	5	US-10-873-846-4	Sequence 4, Appli
18	960	100.0	188	5	US-10-410-897-4	Sequence 4, Appli
19	960	100.0	188	5	US-10-492-261-4	Sequence 4, Appli
20	960	100.0	188	5	US-10-936-447-14	Sequence 14, Appl
21	960	100.0	188	6	US-11-046-440-23	Sequence 23, Appl
22	960	100.0	188	6	US-11-147-492-8	Sequence 8, Appli
23	960	100.0	188	6	US-11-172-549-23	Sequence 23, Appl
24	960	100.0	188	6	US-11-183-205-4	Sequence 4, Appli
25	960	100.0	415	5	US-10-841-250-12	Sequence 12, Appl
26	960	100.0	415	6	US-11-029-003-12	Sequence 12, Appl
27	960	100.0	423	5	US-10-841-250-10	Sequence 10, Appl
28	960	100.0	423	6	US-11-029-003-10	Sequence 10, Appl
29	960	100.0	430	5	US-10-841-250-22	Sequence 22, Appl
30	960	100.0	430	6	US-11-029-003-22	Sequence 22, Appl
31	960	100.0	669	6	US-11-053-100-39	Sequence 39, Appl
32	960	100.0	773	5	US-10-775-180-125	Sequence 125, App
33	960	100.0	773	5	US-10-775-204-403	Sequence 403, App
34	960	100.0	773	6	US-11-175-690-450	Sequence 450, App
35	957	99.7	188	3	US-09-919-622A-7	Sequence 7, Appli
36	957	99.7	188	3	US-09-962-625-1	Sequence 1, Appli
37	957	99.7	188	4	US-10-418-038-7	Sequence 7, Appli
38	957	99.7	188	4	US-10-654-796-1	Sequence 1, Appli
39	957	99.7	188	4	US-10-654-763-1	Sequence 1, Appli
40	957	99.7	188	4	US-10-777-081-1	Sequence 1, Appli
41	957	99.7	188	5	US-10-276-642-8	Sequence 8, Appli
42	957	99.7	188	5	US-10-936-447-16	Sequence 16, Appl
43	957	99.7	188	6	US-11-172-549-21	Sequence 21, Appl
44	957	99.7	188	6	US-11-058-066-22	Sequence 22, Appl
45	955	99.5	188	4	US-10-234-406-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-881-050-24
; Sequence 24, Application US/09881050
; Publication No. US20020025304A1
; GENERAL INFORMATION:
; APPLICANT: CROZE, EDWARD M.
; APPLICANT: FAULDS, DARYL
; APPLICANT: WAGNER, T. CHARIS
; TITLE OF INVENTION: NOVEL INTERFERON FOR THE TREATMENT OF MULTIPLE
; TITLE OF INVENTION: SCLEROSIS
; FILE REFERENCE: BERLX-88
; CURRENT APPLICATION NUMBER: US/09/881,050
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,046
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: IFNalpha2 amino
; OTHER INFORMATION: acid sequence
US-09-881-050-24

Query Match 100.0%; Score 960; DB 3; Length 188;
Best Local Similarity 100.0%; Pred. No. 9.8e-94;
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFG 60

Qy         61 FPQEEFGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEA 120
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Db         61 FPQEEFGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEA 120

Qy        121 CVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNL 180
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Db        121 CVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNL 180

Qy        181 QESLRSKE 188
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RESULT 2
US-09-915-873-4
; Sequence 4, Application US/09915873

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; Publication No. US20020088027A1
; GENERAL INFORMATION:
;  APPLICANT: Stomp, Anne-Marie
;  APPLICANT:  Dickey, Lynn
;  APPLICANT:  Gasdaska, John
;  TITLE OF INVENTION: Expression of Biologically Active
;  TITLE OF INVENTION:  Polypeptides in Duckweed
;  FILE REFERENCE: 40989/237225
;  CURRENT APPLICATION NUMBER: US/09/915,873
;  CURRENT FILING DATE:  2001-07-26
;  PRIOR APPLICATION NUMBER: US 60/293,330
;  PRIOR FILING DATE: 2001-05-23
;  PRIOR APPLICATION NUMBER: US 60/221,705
;  PRIOR FILING DATE: 2000-07-31
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
;   LENGTH: 188
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-915-873-4

  Query Match             100.0%;  Score 960;  DB 3;  Length 188;
  Best Local Similarity   100.0%;  Pred. No. 9.8e-94;
  Matches  188;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy        121 CVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNL 180
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Qy        181 QESLRSKE 188
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Db        181 QESLRSKE 188


RESULT 3
US-10-087-325-2
; Sequence 2, Application US/10087325
; Publication No. US20020192682A1
; GENERAL INFORMATION:
;  APPLICANT: Escary, Jean-Louis
;  TITLE OF INVENTION: NEW POLYNUCLEOTIDES AND POLYPEPTIDES OF THE IFNalpha-2 GENE
;  FILE REFERENCE: 021349/0010
;  CURRENT APPLICATION NUMBER: US/10/087,325
;  CURRENT FILING DATE:  2002-03-01
;  PRIOR APPLICATION NUMBER: FR 0102843
;  PRIOR FILING DATE: 2001-03-01
;  NUMBER OF SEQ ID NOS: 26
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 188
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-087-325-2

  Query Match             100.0%;  Score 960;  DB 4;  Length 188;
  Best Local Similarity   100.0%;  Pred. No. 9.8e-94;
  Matches  188;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFG 60
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Db          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFG 60

Qy         61 FPQEEFGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEA 120
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Qy        121 CVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNL 180
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Db        121 CVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNL 180

Qy        181 QESLRSKE 188
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Db        181 QESLRSKE 188


RESULT 4
US-10-411-037-4
; Sequence 4, Application US/10411037
; Publication No. US20040043446A1
; GENERAL INFORMATION:
;  APPLICANT: Neose Technologies, Inc.
;  APPLICANT:  DeFrees, Shawn
;  APPLICANT:  Zopf, David
;  APPLICANT:  Bayer, Robert
;  APPLICANT:  Hakes, David
;  APPLICANT:  Chen, Xi
;  APPLICANT:  Bowe, Caryn
;  TITLE OF INVENTION: ALPHA GALACTOSIDASE A: REMODELING AND GLYCOCONJUGATION OF ALPHA
;  TITLE OF INVENTION:  GALACTOSIDASE A
;  FILE REFERENCE: 040853-01-5082
;  CURRENT APPLICATION NUMBER: US/10/411,037
;  CURRENT FILING DATE:  2003-04-09
;  PRIOR APPLICATION NUMBER: US 60/328,523
;  PRIOR FILING DATE: 2001-10-10
;  PRIOR APPLICATION NUMBER: US 60/344,692
;  PRIOR FILING DATE: 2001-10-19
;  PRIOR APPLICATION NUMBER: US 60/387,292
;  PRIOR FILING DATE: 2002-06-07
;  PRIOR APPLICATION NUMBER: US 60/391,777
;  PRIOR FILING DATE: 2002-06-25
;  PRIOR APPLICATION NUMBER: US 60/396,594
;  PRIOR FILING DATE: 2002-07-17
;  PRIOR APPLICATION NUMBER: US 60/404,249
;  PRIOR FILING DATE: 2002-08-16
;  PRIOR APPLICATION NUMBER: US 60/407,527
;  PRIOR FILING DATE: 2002-08-28
;  NUMBER OF SEQ ID NOS: 75
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
;   LENGTH: 188
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-411-037-4

  Query Match             100.0%;  Score 960;  DB 4;  Length 188;
  Best Local Similarity   100.0%;  Pred. No. 9.8e-94;
  Matches  188;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFG 60
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Qy         61 FPQEEFGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEA 120
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Qy        121 CVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNL 180
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Db        121 CVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNL 180

Qy        181 QESLRSKE 188
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Db        181 QESLRSKE 188


RESULT 5
US-10-411-026-4
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; Sequence 4, Application US/10411026
; Publication No. US20040063911A1
; GENERAL INFORMATION:
;  APPLICANT: Neose Technologies, Inc.
;  APPLICANT:  DeFrees, Shawn
;  APPLICANT:  Zopf, David
;  APPLICANT:  Bayer, Robert
;  APPLICANT:  Hakes, David
;  APPLICANT:  Chen, Xi
;  TITLE OF INVENTION: PROTEIN REMODELING METHODS AND PROTEINS/PEPTIDES PRODUCED BY THE
;  TITLE OF INVENTION:  METHODS
;  FILE REFERENCE: 040853-01-5053
;  CURRENT APPLICATION NUMBER: US/10/411,026
;  CURRENT FILING DATE:  2003-04-09
;  PRIOR APPLICATION NUMBER: US 60/328,523
;  PRIOR FILING DATE: 2001-10-10
;  PRIOR APPLICATION NUMBER: US 60/344,692
;  PRIOR FILING DATE: 2001-10-19
;  PRIOR APPLICATION NUMBER: US 60/387,292
;  PRIOR FILING DATE: 2002-06-07
;  PRIOR APPLICATION NUMBER: US 60/391,777
;  PRIOR FILING DATE: 2002-06-25
;  PRIOR APPLICATION NUMBER: US 60/396,594
;  PRIOR FILING DATE: 2002-07-17
;  PRIOR APPLICATION NUMBER: US 60/404,249
;  PRIOR FILING DATE: 2002-08-16
;  PRIOR APPLICATION NUMBER: US 60/407,527
;  PRIOR FILING DATE: 2002-08-28
;  NUMBER OF SEQ ID NOS: 75
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
;   LENGTH: 188
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-411-026-4

  Query Match             100.0%;  Score 960;  DB 4;  Length 188;
  Best Local Similarity   100.0%;  Pred. No. 9.8e-94;
  Matches  188;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFG 60
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Db          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFG 60

Qy         61 FPQEEFGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEA 120
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Db         61 FPQEEFGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEA 120

Qy        121 CVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNL 180
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Db        121 CVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNL 180

Qy        181 QESLRSKE 188
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RESULT 6
US-10-410-962-4
; Sequence 4, Application US/10410962
; Publication No. US20040077836A1
; GENERAL INFORMATION:
;  APPLICANT: Neose Technologies, Inc.
;  APPLICANT:  DeFrees, Shawn
;  APPLICANT:  Zopf, David
;  APPLICANT:  Bayer, Robert
;  APPLICANT:  Hakes, David
;  APPLICANT:  Chen, Xi
;  APPLICANT:  Bowe, Caryn
;  TITLE OF INVENTION: GRANULOCYTE COLONY STIMULATING FACTOR: REMODELING AND
;  TITLE OF INVENTION:  GLYCOCONJUGATION OF G-CSF
;  FILE REFERENCE: 040853-01-5054
;  CURRENT APPLICATION NUMBER: US/10/410,962
;  CURRENT FILING DATE:  2003-04-09
;  PRIOR APPLICATION NUMBER: US 60/328,523
;  PRIOR FILING DATE: 2001-10-10
;  PRIOR APPLICATION NUMBER: US 60/344,692
;  PRIOR FILING DATE: 2001-10-19
;  PRIOR APPLICATION NUMBER: US 60/387,292
;  PRIOR FILING DATE: 2002-06-07
;  PRIOR APPLICATION NUMBER: US 60/391,777
;  PRIOR FILING DATE: 2002-06-25
;  PRIOR APPLICATION NUMBER: US 60/396,594
;  PRIOR FILING DATE: 2002-07-17
;  PRIOR APPLICATION NUMBER: US 60/404,249
;  PRIOR FILING DATE: 2002-08-16
;  PRIOR APPLICATION NUMBER: US 60/407,527
;  PRIOR FILING DATE: 2002-08-28
;  NUMBER OF SEQ ID NOS: 75
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
;   LENGTH: 188
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-410-962-4

  Query Match             100.0%;  Score 960;  DB 4;  Length 188;
  Best Local Similarity   100.0%;  Pred. No. 9.8e-94;
  Matches  188;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFG 60
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Qy        121 CVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNL 180
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Db        121 CVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNL 180

Qy        181 QESLRSKE 188
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Db        181 QESLRSKE 188


RESULT 7
US-10-411-049-4
; Sequence 4, Application US/10411049
; Publication No. US20040082026A1
; GENERAL INFORMATION:
;  APPLICANT: Neose Technologies, Inc.
;  APPLICANT:  DeFrees, Shawn
;  APPLICANT:  Zopf, David
;  APPLICANT:  Bayer, Robert
;  APPLICANT:  Hakes, David
;  APPLICANT:  Chen, Xi
;  APPLICANT:  Bowe, Caryn
;  TITLE OF INVENTION: INTERFERON ALPHA: REMODELING AND GLYCOCONJUGATION OF INTERFERON
;  TITLE OF INVENTION:  ALPHA
;  FILE REFERENCE: 040853-01-5055
;  CURRENT APPLICATION NUMBER: US/10/411,049
;  CURRENT FILING DATE:  2003-04-09
;  PRIOR APPLICATION NUMBER: US 60/328,523
;  PRIOR FILING DATE: 2001-10-10
;  PRIOR APPLICATION NUMBER: US 60/344,692
;  PRIOR FILING DATE: 2001-10-19
;  PRIOR APPLICATION NUMBER: US 60/387,292
;  PRIOR FILING DATE: 2002-06-07
;  PRIOR APPLICATION NUMBER: US 60/391,777
;  PRIOR FILING DATE: 2002-06-25
;  PRIOR APPLICATION NUMBER: US 60/396,594
;  PRIOR FILING DATE: 2002-07-17
;  PRIOR APPLICATION NUMBER: US 60/404,249
;  PRIOR FILING DATE: 2002-08-16
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;  PRIOR APPLICATION NUMBER: US 60/407,527
;  PRIOR FILING DATE: 2002-08-28
;  NUMBER OF SEQ ID NOS: 75
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
;   LENGTH: 188
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-411-049-4

  Query Match             100.0%;  Score 960;  DB 4;  Length 188;
  Best Local Similarity   100.0%;  Pred. No. 9.8e-94;
  Matches  188;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFG 60

Qy         61 FPQEEFGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FPQEEFGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEA 120

Qy        121 CVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNL 180

Qy        181 QESLRSKE 188
              ||||||||
Db        181 QESLRSKE 188


RESULT 8
US-10-410-930-4
; Sequence 4, Application US/10410930
; Publication No. US20040115168A1
; GENERAL INFORMATION:
;  APPLICANT: Neose Technologies, Inc.
;  APPLICANT:  DeFrees, Shawn
;  APPLICANT:  Zopf, David
;  APPLICANT:  Bayer, Robert
;  APPLICANT:  Hakes, David
;  APPLICANT:  Chen, Xi
;  APPLICANT:  Bowe, Caryn
;  TITLE OF INVENTION: INTERFERON BETA: REMODELING AND GLYCOCONJUGATION OF INTERFERON
;  TITLE OF INVENTION:  BETA
;  FILE REFERENCE: 040853-01-5056
;  CURRENT APPLICATION NUMBER: US/10/410,930
;  CURRENT FILING DATE:  2003-04-09
;  PRIOR APPLICATION NUMBER: US 60/328,523
;  PRIOR FILING DATE: 2001-10-10
;  PRIOR APPLICATION NUMBER: US 60/344,692
;  PRIOR FILING DATE: 2001-10-19
;  PRIOR APPLICATION NUMBER: US 60/387,292
;  PRIOR FILING DATE: 2002-06-07
;  PRIOR APPLICATION NUMBER: US 60/391,777
;  PRIOR FILING DATE: 2002-06-25
;  PRIOR APPLICATION NUMBER: US 60/396,594
;  PRIOR FILING DATE: 2002-07-17
;  PRIOR APPLICATION NUMBER: US 60/404,249
;  PRIOR FILING DATE: 2002-08-16
;  PRIOR APPLICATION NUMBER: US 60/407,527
;  PRIOR FILING DATE: 2002-08-28
;  NUMBER OF SEQ ID NOS: 75
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
;   LENGTH: 188
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-410-930-4

  Query Match             100.0%;  Score 960;  DB 4;  Length 188;
  Best Local Similarity   100.0%;  Pred. No. 9.8e-94;
  Matches  188;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFG 60

Qy         61 FPQEEFGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FPQEEFGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEA 120

Qy        121 CVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNL 180

Qy        181 QESLRSKE 188
              ||||||||
Db        181 QESLRSKE 188


RESULT 9
US-10-410-997-4
; Sequence 4, Application US/10410997
; Publication No. US20040126838A1
; GENERAL INFORMATION:
;  APPLICANT: Neose Technologies, Inc.
;  APPLICANT:  DeFrees, Shawn
;  APPLICANT:  Zopf, David
;  APPLICANT:  Bayer, Robert
;  APPLICANT:  Hakes, David
;  APPLICANT:  Chen, Xi
;  APPLICANT:  Bowe, Caryn
;  TITLE OF INVENTION: FOLLICLE STIMULATING HORMONE: REMODELING AND GLYCOCONJUGATION OF
;  TITLE OF INVENTION:  FSH
;  FILE REFERENCE: 040853-01-5059
;  CURRENT APPLICATION NUMBER: US/10/410,997
;  CURRENT FILING DATE:  2003-04-09
;  PRIOR APPLICATION NUMBER: US 60/328,523
;  PRIOR FILING DATE: 2001-10-10
;  PRIOR APPLICATION NUMBER: US 60/344,692
;  PRIOR FILING DATE: 2001-10-19
;  PRIOR APPLICATION NUMBER: US 60/387,292
;  PRIOR FILING DATE: 2002-06-07
;  PRIOR APPLICATION NUMBER: US 60/391,777
;  PRIOR FILING DATE: 2002-06-25
;  PRIOR APPLICATION NUMBER: US 60/396,594
;  PRIOR FILING DATE: 2002-07-17
;  PRIOR APPLICATION NUMBER: US 60/404,249
;  PRIOR FILING DATE: 2002-08-16
;  PRIOR APPLICATION NUMBER: US 60/407,527
;  PRIOR FILING DATE: 2002-08-28
;  NUMBER OF SEQ ID NOS: 75
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
;   LENGTH: 188
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-410-997-4

  Query Match             100.0%;  Score 960;  DB 4;  Length 188;
  Best Local Similarity   100.0%;  Pred. No. 9.8e-94;
  Matches  188;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFG 60

Qy         61 FPQEEFGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FPQEEFGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEA 120

Qy        121 CVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNL 180
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Qy        181 QESLRSKE 188
              ||||||||
Db        181 QESLRSKE 188


RESULT 10
US-10-411-012-4
; Sequence 4, Application US/10411012
; Publication No. US20040132640A1
; GENERAL INFORMATION:
;  APPLICANT: Neose Technologies, Inc.
;  APPLICANT:  DeFrees, Shawn
;  APPLICANT:  Zopf, David
;  APPLICANT:  Bayer, Robert
;  APPLICANT:  Hakes, David
;  APPLICANT:  Chen, Xi
;  APPLICANT:  Bowe, Caryne
;  TITLE OF INVENTION: GLYCOPEGYLATION METHODS AND PROTEINS/PEPTIDES PRODUCED BY THE
;  TITLE OF INVENTION:  METHODS
;  FILE REFERENCE: 040853-01-5051
;  CURRENT APPLICATION NUMBER: US/10/411,012
;  CURRENT FILING DATE:  2003-04-09
;  PRIOR APPLICATION NUMBER: US 60/328,523
;  PRIOR FILING DATE: 2001-10-10
;  PRIOR APPLICATION NUMBER: US 60/344,692
;  PRIOR FILING DATE: 2001-10-19
;  PRIOR APPLICATION NUMBER: US 60/387,292
;  PRIOR FILING DATE: 2002-06-07
;  PRIOR APPLICATION NUMBER: US 60/391,777
;  PRIOR FILING DATE: 2002-06-25
;  PRIOR APPLICATION NUMBER: US 60/396,594
;  PRIOR FILING DATE: 2002-07-17
;  PRIOR APPLICATION NUMBER: US 60/404,249
;  PRIOR FILING DATE: 2002-08-16
;  PRIOR APPLICATION NUMBER: US 60/407,527
;  PRIOR FILING DATE: 2002-08-28
;  NUMBER OF SEQ ID NOS: 75
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
;   LENGTH: 188
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-411-012-4

  Query Match             100.0%;  Score 960;  DB 4;  Length 188;
  Best Local Similarity   100.0%;  Pred. No. 9.8e-94;
  Matches  188;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFG 60

Qy         61 FPQEEFGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FPQEEFGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEA 120

Qy        121 CVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNL 180
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Db        121 CVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNL 180

Qy        181 QESLRSKE 188
              ||||||||
Db        181 QESLRSKE 188


RESULT 11
US-10-287-994-4
; Sequence 4, Application US/10287994
; Publication No. US20040137557A1
; GENERAL INFORMATION:
;  APPLICANT: Neose Technologies, Inc.
;  APPLICANT:  DeFrees, Shawn
;  APPLICANT:  Zopf, David
;  APPLICANT:  Bayer, Robert
;  APPLICANT:  Bowe, Caryn
;  APPLICANT:  Hakes, David
;  APPLICANT:  Chen, Xi
;  TITLE OF INVENTION: REMODELING AND GLYCOCONJUGATION OF PEPTIDES
;  FILE REFERENCE: 040853-01-5052-00
;  CURRENT APPLICATION NUMBER: US/10/287,994
;  CURRENT FILING DATE:  2002-11-05
;  PRIOR APPLICATION NUMBER: US 60/328,523
;  PRIOR FILING DATE: 2001-10-10
;  PRIOR APPLICATION NUMBER: US 60/344,692
;  PRIOR FILING DATE: 2001-10-19
;  PRIOR APPLICATION NUMBER: US 60/387,292
;  PRIOR FILING DATE: 2002-06-07
;  PRIOR APPLICATION NUMBER: US 60/391,777
;  PRIOR FILING DATE: 2002-06-25
;  PRIOR APPLICATION NUMBER: US 60/396,594
;  PRIOR FILING DATE: 2002-07-17
;  PRIOR APPLICATION NUMBER: US 60/404,249
;  PRIOR FILING DATE: 2002-08-16
;  PRIOR APPLICATION NUMBER: US 60/407,527
;  PRIOR FILING DATE: 2002-08-28
;  NUMBER OF SEQ ID NOS: 62
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
;   LENGTH: 188
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-287-994-4

  Query Match             100.0%;  Score 960;  DB 4;  Length 188;
  Best Local Similarity   100.0%;  Pred. No. 9.8e-94;
  Matches  188;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFG 60
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Db          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFG 60

Qy         61 FPQEEFGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FPQEEFGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEA 120

Qy        121 CVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNL 180
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Db        121 CVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNL 180

Qy        181 QESLRSKE 188
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Db        181 QESLRSKE 188


RESULT 12
US-10-410-913-4
; Sequence 4, Application US/10410913
; Publication No. US20040142856A1
; GENERAL INFORMATION:
;  APPLICANT: Neose Technologies, Inc.
;  APPLICANT:  DeFrees, Shawn
;  APPLICANT:  Zopf, David
;  APPLICANT:  Bayer, Robert
;  APPLICANT:  Hakes, David
;  APPLICANT:  Chen, Xi
;  APPLICANT:  Bowe, Caryn
;  TITLE OF INVENTION: GLYCOCONJUGATION METHODS AND PROTEINS/PEPTIDES PRODUCED BY THE
;  TITLE OF INVENTION:  METHODS
;  FILE REFERENCE: 040853-01-5081
;  CURRENT APPLICATION NUMBER: US/10/410,913
;  CURRENT FILING DATE:  2003-04-09
;  PRIOR APPLICATION NUMBER: US 60/328,523
;  PRIOR FILING DATE: 2001-10-10
;  PRIOR APPLICATION NUMBER: US 60/344,692
;  PRIOR FILING DATE: 2001-10-19
;  PRIOR APPLICATION NUMBER: US 60/387,292
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;  PRIOR FILING DATE: 2002-06-07
;  PRIOR APPLICATION NUMBER: US 60/391,777
;  PRIOR FILING DATE: 2002-06-25
;  PRIOR APPLICATION NUMBER: US 60/396,594
;  PRIOR FILING DATE: 2002-07-17
;  PRIOR APPLICATION NUMBER: US 60/404,249
;  PRIOR FILING DATE: 2002-08-16
;  PRIOR APPLICATION NUMBER: US 60/407,527
;  PRIOR FILING DATE: 2002-08-28
;  NUMBER OF SEQ ID NOS: 75
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
;   LENGTH: 188
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-410-913-4

  Query Match             100.0%;  Score 960;  DB 4;  Length 188;
  Best Local Similarity   100.0%;  Pred. No. 9.8e-94;
  Matches  188;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFG 60
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Db          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFG 60

Qy         61 FPQEEFGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FPQEEFGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEA 120

Qy        121 CVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNL 180

Qy        181 QESLRSKE 188
              ||||||||
Db        181 QESLRSKE 188


RESULT 13
US-10-276-642-12
; Sequence 12, Application US/10276642
; Publication No. US20040235156A1
; GENERAL INFORMATION:
;  APPLICANT: Ralph, Stephen John
;  TITLE OF INVENTION: IMMUNE POTENTIATING COMPOSITIONS
;  FILE REFERENCE: DAVI200.001APC
;  CURRENT APPLICATION NUMBER: US/10/276,642
;  CURRENT FILING DATE:  2002-11-15
;  PRIOR APPLICATION NUMBER: PCT/AU01/00565
;  PRIOR FILING DATE: 2001-05-17
;  PRIOR APPLICATION NUMBER: PQ 7553
;  PRIOR FILING DATE: 2000-05-17
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12
;   LENGTH: 188
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-276-642-12

  Query Match             100.0%;  Score 960;  DB 5;  Length 188;
  Best Local Similarity   100.0%;  Pred. No. 9.8e-94;
  Matches  188;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFG 60
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Db          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFG 60

Qy         61 FPQEEFGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FPQEEFGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEA 120

Qy        121 CVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNL 180

Qy        181 QESLRSKE 188
              ||||||||
Db        181 QESLRSKE 188


RESULT 14
US-10-794-615-4
; Sequence 4, Application US/10794615
; Publication No. US20040261148A1
; GENERAL INFORMATION:
;  APPLICANT: Dickey, Lynn
;  APPLICANT:  Gasdaska, John
;  APPLICANT:  Cox, Kevin
;  TITLE OF INVENTION: Expression of Biologically Active
;  TITLE OF INVENTION:  Polypeptides in Duckweed
;  FILE REFERENCE: 40989/267934
;  CURRENT APPLICATION NUMBER: US/10/794,615
;  CURRENT FILING DATE:  2004-03-05
;  PRIOR APPLICATION NUMBER: US/10/675,011
;  PRIOR FILING DATE: 2003-09-30
;  PRIOR APPLICATION NUMBER: US 09/915,873
;  PRIOR FILING DATE: 2001-07-26
;  PRIOR APPLICATION NUMBER: US 60/293,330
;  PRIOR FILING DATE: 2001-05-23
;  PRIOR APPLICATION NUMBER: US 60/221,705
;  PRIOR FILING DATE: 2000-07-31
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
;   LENGTH: 188
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-794-615-4

  Query Match             100.0%;  Score 960;  DB 5;  Length 188;
  Best Local Similarity   100.0%;  Pred. No. 9.8e-94;
  Matches  188;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFG 60

Qy         61 FPQEEFGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FPQEEFGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEA 120

Qy        121 CVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNL 180

Qy        181 QESLRSKE 188
              ||||||||
Db        181 QESLRSKE 188


RESULT 15
US-10-653-350-1
; Sequence 1, Application US/10653350
; Publication No. US20050019871A1
; GENERAL INFORMATION:
;  APPLICANT: Lee, Eun Jung
;  APPLICANT:  Park, Hyung Ki
;  APPLICANT:  Park, Ji Sook
;  APPLICANT:  Kim, Yeon Hyang
;  APPLICANT:  Lee, Hyune Soo
;  APPLICANT:  Koh, Hyung Kon
;  APPLICANT:  Oh, Myung Suk
;  TITLE OF INVENTION: GLYCOSYLATED HUMAN INTERFERON ALPHA
;  TITLE OF INVENTION:  ISOFORM
;  FILE REFERENCE: A35967  073226.0119
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;  CURRENT APPLICATION NUMBER: US/10/653,350
;  CURRENT FILING DATE:  2003-09-02
;  PRIOR APPLICATION NUMBER: KR 10-2002-0052365
;  PRIOR FILING DATE: 2002-08-31
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 188
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Human interferon alpha isoform
;   FEATURE:
;   NAME/KEY: SIGNAL
;   LOCATION: (1)...(23)
;   OTHER INFORMATION: Propeptide
US-10-653-350-1

  Query Match             100.0%;  Score 960;  DB 5;  Length 188;
  Best Local Similarity   100.0%;  Pred. No. 9.8e-94;
  Matches  188;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFG 60

Qy         61 FPQEEFGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FPQEEFGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEA 120

Qy        121 CVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNL 180

Qy        181 QESLRSKE 188
              ||||||||
Db        181 QESLRSKE 188

Search completed: October 14, 2006, 08:06:40
Job time : 180 secs
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GenCore version 5.1.9

OM protein - protein search, using sw model

Run on: October 14, 2006, 08:03:47 ; Search time 39 Seconds
(without alignments)
382.774 Million cell updates/sec

Title: US-10-653-350-1
Perfect score: 960
Sequence: 1 MALTFALLVALLVLSCKSSC.....EIMRSFSLSTNLQESLRSKE 188

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 295242 seqs, 79405279 residues

Total number of hits satisfying chosen parameters: 295242

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_New:*
1: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
8: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

** Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	960	100.0	188	6	US-10-675-011-4	Sequence 4, Appli
2	960	100.0	188	7	US-11-183-218-4	Sequence 4, Appli
3	960	100.0	773	7	US-11-429-276-403	Sequence 403, App
4	867	90.3	201	7	US-11-036-257-79	Sequence 79, Appl
5	867	90.3	231	7	US-11-036-257-85	Sequence 85, Appl
6	863	89.9	209	7	US-11-036-257-65	Sequence 65, Appl
7	860.5	89.6	196	7	US-11-036-257-83	Sequence 83, Appl
8	860.5	89.6	206	7	US-11-036-257-81	Sequence 81, Appl
9	859	89.5	192	6	US-10-568-332-14	Sequence 14, Appl
10	856	89.2	774	7	US-11-429-276-352	Sequence 352, App
11	855.5	89.1	226	7	US-11-036-257-87	Sequence 87, Appl
12	855.5	89.1	769	7	US-11-429-276-386	Sequence 386, App
13	855.5	89.1	769	7	US-11-429-276-407	Sequence 407, App
14	853.5	88.9	774	7	US-11-429-276-402	Sequence 402, App
15	853.5	88.9	774	7	US-11-429-276-1300	Sequence 1300, Ap
16	851	88.6	165	6	US-10-675-011-5	Sequence 5, Appli
17	851	88.6	165	7	US-11-370-555-30	Sequence 30, Appl
18	851	88.6	165	7	US-11-330-917-1	Sequence 1, Appli
19	851	88.6	165	7	US-11-363-637-30	Sequence 30, Appl
20	851	88.6	165	7	US-11-429-276-568	Sequence 568, App
21	851	88.6	165	7	US-11-429-276-602	Sequence 602, App
22	851	88.6	165	7	US-11-429-276-613	Sequence 613, App
23	851	88.6	165	7	US-11-429-276-618	Sequence 618, App
24	851	88.6	165	7	US-11-429-276-619	Sequence 619, App
25	851	88.6	165	7	US-11-429-276-623	Sequence 623, App
26	851	88.6	165	7	US-11-429-276-1302	Sequence 1302, Ap
27	851	88.6	165	7	US-11-351-163-1	Sequence 1, Appli
28	851	88.6	166	6	US-10-933-854-12	Sequence 12, Appl
29	851	88.6	166	7	US-11-351-163-1357	Sequence 1357, Ap
30	851	88.6	539	7	US-11-244-349B-37	Sequence 37, Appl
31	851	88.6	835	7	US-11-429-276-397	Sequence 397, App
32	849	88.4	165	7	US-11-330-917-84	Sequence 84, Appl
33	849	88.4	165	7	US-11-330-917-103	Sequence 103, App
34	849	88.4	165	7	US-11-330-917-109	Sequence 109, App
35	849	88.4	165	7	US-11-351-163-84	Sequence 84, Appl
36	849	88.4	165	7	US-11-351-163-103	Sequence 103, App
37	849	88.4	165	7	US-11-351-163-109	Sequence 109, App
38	848	88.3	165	7	US-11-330-917-7	Sequence 7, Appli
39	848	88.3	165	7	US-11-330-917-10	Sequence 10, Appl
40	848	88.3	165	7	US-11-330-917-20	Sequence 20, Appl
41	848	88.3	165	7	US-11-330-917-22	Sequence 22, Appl
42	848	88.3	165	7	US-11-330-917-54	Sequence 54, Appl
43	848	88.3	165	7	US-11-330-917-72	Sequence 72, Appl
44	848	88.3	165	7	US-11-330-917-76	Sequence 76, Appl
45	848	88.3	165	7	US-11-330-917-87	Sequence 87, Appl

ALIGNMENTS

RESULT 1
US-10-675-011-4
; Sequence 4, Application US/10675011
; Publication No. US20060195946A1
; GENERAL INFORMATION:
; APPLICANT: Dickey, Lynn
; APPLICANT: Gasdaska, John
; APPLICANT: Cox, Kevin
; TITLE OF INVENTION: Expression of Biologically Active
; TITLE OF INVENTION: Polypeptides in Duckweed
; FILE REFERENCE: 40989/267934
; CURRENT APPLICATION NUMBER: US/10/675,011
; CURRENT FILING DATE: 2003-09-30
; PRIOR APPLICATION NUMBER: US 09/915,873
; PRIOR FILING DATE: 2001-07-26
; PRIOR APPLICATION NUMBER: US 60/293,330
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/221,705
; PRIOR FILING DATE: 2000-07-31
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-675-011-4

Query Match 100.0%; Score 960; DB 6; Length 188;
Best Local Similarity 100.0%; Pred. No. 8.7e-86;
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFG 60
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Db          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFG 60

Qy         61 FPQEEFGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEA 120
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Db         61 FPQEEFGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEA 120

Qy        121 CVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNL 180

Qy        181 QESLRSKE 188
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Db        181 QESLRSKE 188
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RESULT 2
US-11-183-218-4
; Sequence 4, Application US/11183218
; Publication No. US20060088906A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: DeFrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bowe, Caryne
; TITLE OF INVENTION: ERYTHROPOIETIN: REMODELING AND
; TITLE OF INVENTION: GLYCOCONJUGATION OF ERYTHROPOIETIN
; FILE REFERENCE: 040853-01-5083-US02
; CURRENT APPLICATION NUMBER: US/11/183,218
; CURRENT FILING DATE: 2005-07-15
; PRIOR APPLICATION NUMBER: US 10/410,945
; PRIOR FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: PCT/US02/32263
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: US 60/334,301
; PRIOR FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: US 60/334,233
; PRIOR FILING DATE: 2001-11-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-183-218-4

Query Match 100.0%; Score 960; DB 7; Length 188;
Best Local Similarity 100.0%; Pred. No. 8.7e-86;
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFG 60
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Db          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFG 60

Qy         61 FPQEEFGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEA 120
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Db         61 FPQEEFGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEA 120

Qy        121 CVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNL 180
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Db        121 CVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNL 180

Qy        181 QESLRSKE 188
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Db        181 QESLRSKE 188
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RESULT 3
US-11-429-276-403
; Sequence 403, Application US/11429276
; Publication No. US20060194735A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF564
; CURRENT APPLICATION NUMBER: US/11/429,276
; CURRENT FILING DATE: 2006-05-08
; PRIOR APPLICATION NUMBER: 10/775,204
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: PCT/US02/40891
; PRIOR FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: 60/341,811
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/360,000
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: 60/378,950
; PRIOR FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: 60/398,008
; PRIOR FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: 60/411,355
; PRIOR FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: 60/414,984
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: 60/417,611
; PRIOR FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: 60/420,246
; PRIOR FILING DATE: 2002-10-23
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2222
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 403
; LENGTH: 773
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-429-276-403

Query Match 100.0%; Score 960; DB 7; Length 773;
Best Local Similarity 100.0%; Pred. No. 5e-85;
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFG 60

Qy         61 FPQEEFGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEA 120
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Db         61 FPQEEFGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEA 120

Qy        121 CVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNL 180
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Db        121 CVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNL 180

Qy        181 QESLRSKE 188
              ||||||||
Db        181 QESLRSKE 188
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RESULT 4
US-11-036-257-79
; Sequence 79, Application US/11036257
; Publication No. US20060148680A1
; GENERAL INFORMATION:
; APPLICANT: KIELISZEWSKI, MARCIA
; APPLICANT: XU, JIANFENG
; APPLICANT: KOPCHICK, JOHN J.
; APPLICANT: OKADA, SHIGERU
; TITLE OF INVENTION: GLYCOPROTEINS PRODUCED IN PLANTS AND METHODS OF
; TITLE OF INVENTION: THEIR USE
; FILE REFERENCE: 27211/04081
; CURRENT APPLICATION NUMBER: US/11/036,257
; CURRENT FILING DATE: 2005-01-14
; PRIOR APPLICATION NUMBER: 60/602,562
; PRIOR FILING DATE: 2004-08-18
; PRIOR APPLICATION NUMBER: 60/582,027
; PRIOR FILING DATE: 2004-06-22
; PRIOR APPLICATION NUMBER: 60/536,486

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;  PRIOR FILING DATE: 2004-01-14
;  NUMBER OF SEQ ID NOS: 173
;  SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 79
;   LENGTH: 201
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: amino acid construct
US-11-036-257-79

  Query Match             90.3%;  Score 867;  DB 7;  Length 201;
  Best Local Similarity   91.0%;  Pred. No. 1e-76;
  Matches  171;  Conservative    4;  Mismatches   13;  Indels    0;  Gaps    0;

Qy          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFG 60
              ||  ||  : :||    :  :  |||||||||||||||||||||||||||||||||||||
Db          4 MASLFATFLVVLVSLSLAQTTRACDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFG 63

Qy         61 FPQEEFGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEA 120
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Db         64 FPQEEFGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEA 123

Qy        121 CVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNL 180
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Db        124 CVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNL 183

Qy        181 QESLRSKE 188
              ||||||||
Db        184 QESLRSKE 191


RESULT 5
US-11-036-257-85
; Sequence 85, Application US/11036257
; Publication No. US20060148680A1
; GENERAL INFORMATION:
;  APPLICANT: KIELISZEWSKI, MARCIA
;  APPLICANT:  XU, JIANFENG
;  APPLICANT:  KOPCHICK, JOHN J.
;  APPLICANT:  OKADA, SHIGERU
;  TITLE OF INVENTION: GLYCOPROTEINS PRODUCED IN PLANTS AND METHODS OF
;  TITLE OF INVENTION:  THEIR USE
;  FILE REFERENCE: 27211/04081
;  CURRENT APPLICATION NUMBER: US/11/036,257
;  CURRENT FILING DATE:  2005-01-14
;  PRIOR APPLICATION NUMBER: 60/602,562
;  PRIOR FILING DATE: 2004-08-18
;  PRIOR APPLICATION NUMBER: 60/582,027
;  PRIOR FILING DATE: 2004-06-22
;  PRIOR APPLICATION NUMBER: 60/536,486
;  PRIOR FILING DATE: 2004-01-14
;  NUMBER OF SEQ ID NOS: 173
;  SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 85
;   LENGTH: 231
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: amino acid construct
US-11-036-257-85

  Query Match             90.3%;  Score 867;  DB 7;  Length 231;
  Best Local Similarity   91.0%;  Pred. No. 1.2e-76;
  Matches  171;  Conservative    4;  Mismatches   13;  Indels    0;  Gaps    0;

Qy          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFG 60
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Db          4 MASLFATFLVVLVSLSLAQTTRACDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFG 63

Qy         61 FPQEEFGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEA 120
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Db         64 FPQEEFGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEA 123

Qy        121 CVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNL 180
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Db        124 CVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNL 183

Qy        181 QESLRSKE 188
              ||||||||
Db        184 QESLRSKE 191


RESULT 6
US-11-036-257-65
; Sequence 65, Application US/11036257
; Publication No. US20060148680A1
; GENERAL INFORMATION:
;  APPLICANT: KIELISZEWSKI, MARCIA
;  APPLICANT:  XU, JIANFENG
;  APPLICANT:  KOPCHICK, JOHN J.
;  APPLICANT:  OKADA, SHIGERU
;  TITLE OF INVENTION: GLYCOPROTEINS PRODUCED IN PLANTS AND METHODS OF
;  TITLE OF INVENTION:  THEIR USE
;  FILE REFERENCE: 27211/04081
;  CURRENT APPLICATION NUMBER: US/11/036,257
;  CURRENT FILING DATE:  2005-01-14
;  PRIOR APPLICATION NUMBER: 60/602,562
;  PRIOR FILING DATE: 2004-08-18
;  PRIOR APPLICATION NUMBER: 60/582,027
;  PRIOR FILING DATE: 2004-06-22
;  PRIOR APPLICATION NUMBER: 60/536,486
;  PRIOR FILING DATE: 2004-01-14
;  NUMBER OF SEQ ID NOS: 173
;  SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 65
;   LENGTH: 209
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: amino acid construct
US-11-036-257-65

  Query Match             89.9%;  Score 863;  DB 7;  Length 209;
  Best Local Similarity   92.0%;  Pred. No. 2.6e-76;
  Matches  173;  Conservative    1;  Mismatches   12;  Indels    2;  Gaps    1;

Qy          1 MALTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFG 60
              ||  ||    |:||   |     |||||||||||||||||||||||||||||||||||||
Db          4 MASLFATF--LVVLVSLSLAQTTCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFG 61

Qy         61 FPQEEFGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 FPQEEFGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEA 121

Qy        121 CVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 CVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNL 181

Qy        181 QESLRSKE 188
              ||||||||
Db        182 QESLRSKE 189


RESULT 7
US-11-036-257-83
; Sequence 83, Application US/11036257
; Publication No. US20060148680A1
; GENERAL INFORMATION:
;  APPLICANT: KIELISZEWSKI, MARCIA
;  APPLICANT:  XU, JIANFENG
;  APPLICANT:  KOPCHICK, JOHN J.
;  APPLICANT:  OKADA, SHIGERU
```

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;  TITLE OF INVENTION: GLYCOPROTEINS PRODUCED IN PLANTS AND METHODS OF
;  TITLE OF INVENTION:  THEIR USE
;  FILE REFERENCE: 27211/04081
;  CURRENT APPLICATION NUMBER: US/11/036,257
;  CURRENT FILING DATE:  2005-01-14
;  PRIOR APPLICATION NUMBER: 60/602,562
;  PRIOR FILING DATE: 2004-08-18
;  PRIOR APPLICATION NUMBER: 60/582,027
;  PRIOR FILING DATE: 2004-06-22
;  PRIOR APPLICATION NUMBER: 60/536,486
;  PRIOR FILING DATE: 2004-01-14
;  NUMBER OF SEQ ID NOS: 173
;  SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 83
;   LENGTH: 196
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: amino acid construct
US-11-036-257-83

  Query Match             89.6%;  Score 860.5;  DB 7;  Length 196;
  Best Local Similarity   89.6%;  Pred. No. 4.2e-76;
  Matches  173;  Conservative    3;  Mismatches   12;  Indels    5;  Gaps    1;

Qy          1 MALTFALLVALLVLSCKSSCSVG-----CDLPQTHSLGSRRTLMLLAQMRRISLFSCLKD 55
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Db          4 MASLFATFLVVLVSLSLASPSPSPSPSPCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKD 63

Qy         56 RHDFGFPQEEFGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQL 115
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 RHDFGFPQEEFGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQL 123

Qy        116 NDLEACVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFS 175
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 NDLEACVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFS 183

Qy        176 LSTNLQESLRSKE 188
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Db        184 LSTNLQESLRSKE 196


RESULT 8
US-11-036-257-81
; Sequence 81, Application US/11036257
; Publication No. US20060148680A1
; GENERAL INFORMATION:
;  APPLICANT: KIELISZEWSKI, MARCIA
;  APPLICANT:  XU, JIANFENG
;  APPLICANT:  KOPCHICK, JOHN J.
;  APPLICANT:  OKADA, SHIGERU
;  TITLE OF INVENTION: GLYCOPROTEINS PRODUCED IN PLANTS AND METHODS OF
;  TITLE OF INVENTION:  THEIR USE
;  FILE REFERENCE: 27211/04081
;  CURRENT APPLICATION NUMBER: US/11/036,257
;  CURRENT FILING DATE:  2005-01-14
;  PRIOR APPLICATION NUMBER: 60/602,562
;  PRIOR FILING DATE: 2004-08-18
;  PRIOR APPLICATION NUMBER: 60/582,027
;  PRIOR FILING DATE: 2004-06-22
;  PRIOR APPLICATION NUMBER: 60/536,486
;  PRIOR FILING DATE: 2004-01-14
;  NUMBER OF SEQ ID NOS: 173
;  SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 81
;   LENGTH: 206
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: amino acid construct
US-11-036-257-81

  Query Match             89.6%;  Score 860.5;  DB 7;  Length 206;
  Best Local Similarity   89.6%;  Pred. No. 4.5e-76;
  Matches  173;  Conservative    3;  Mismatches   12;  Indels    5;  Gaps    1;

Qy          1 MALTFALLVALLVLSCKSSCSVG-----CDLPQTHSLGSRRTLMLLAQMRRISLFSCLKD 55
              ||  ||  : :||    :| |       |||||||||||||||||||||||||||||||
Db          4 MASLFATFLVVLVSLSLASPSPSPSPSPCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKD 63

Qy         56 RHDFGFPQEEFGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQL 115
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 RHDFGFPQEEFGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQL 123

Qy        116 NDLEACVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFS 175
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 NDLEACVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFS 183

Qy        176 LSTNLQESLRSKE 188
              |||||||||||||
Db        184 LSTNLQESLRSKE 196


RESULT 9
US-10-568-332-14
; Sequence 14, Application US/10568332
; Publication No. US20060173167A1
; GENERAL INFORMATION:
;  APPLICANT: Stempfer, Gunter
;  APPLICANT:  Alliger, Peter
;  APPLICANT:  Palma, Norbert
;  TITLE OF INVENTION: Process for the purification of recombinant polypeptides
;  FILE REFERENCE: BP/G-33315A LNG 61310.US
;  CURRENT APPLICATION NUMBER: US/10/568,332
;  CURRENT FILING DATE:  2006-02-13
;  PRIOR APPLICATION NUMBER: PCT/EP2004/009055
;  PRIOR FILING DATE: 2004-08-12
;  PRIOR APPLICATION NUMBER: US 60/494,915
;  PRIOR FILING DATE: 2003-08-13
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 14
;   LENGTH: 192
;   TYPE: PRT
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Synthetic Construct
US-10-568-332-14

  Query Match             89.5%;  Score 859;  DB 6;  Length 192;
  Best Local Similarity   92.8%;  Pred. No. 5.8e-76;
  Matches  168;  Conservative    3;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          8 LVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFGFPQEEFG 67
              ||   |:    : : |||||||||||||||||||||||||||||||||||||||||||||
Db         12 LVMATVIGLAPAVAFACDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFGFPQEEFG 71

Qy         68 NQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEACVIQGVG 127
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         72 NQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEACVIQGVG 131

Qy        128 VTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNLQESLRSK 187
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        132 VTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNLQESLRSK 191

Qy        188 E 188
              |
Db        192 E 192


RESULT 10
US-11-429-276-352
; Sequence 352, Application US/11429276
; Publication No. US20060194735A1
```

; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF564
; CURRENT APPLICATION NUMBER: US/11/429,276
; CURRENT FILING DATE: 2006-05-08
; PRIOR APPLICATION NUMBER: 10/775,204
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: PCT/US02/40891
; PRIOR FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: 60/341,811
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/360,000
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: 60/378,950
; PRIOR FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: 60/398,008
; PRIOR FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: 60/411,355
; PRIOR FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: 60/414,984
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: 60/417,611
; PRIOR FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: 60/420,246
; PRIOR FILING DATE: 2002-10-23
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2222
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 352
; LENGTH: 774
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-429-276-352

Query Match 89.2%; Score 856; DB 7; Length 774;
Best Local Similarity 90.9%; Pred. No. 6.3e-75;
Matches 169; Conservative 4; Mismatches 13; Indels 0; Gaps 0;

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Qy          3 LTFALLVALLVLSCKSSCSVGCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFGFP 62
              ::|  |: |   :   |    ||||||||||||||||||||||||||||||||||||||
Db          4 VSFISLLFLFSSAYSRSLDKRCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFGFP 63

Qy         63 QEEFGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEACV 122
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 QEEFGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEACV 123

Qy        123 IQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNLQE 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 IQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNLQE 183

Qy        183 SLRSKE 188
              ||||||
Db        184 SLRSKE 189
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RESULT 11
US-11-036-257-87
; Sequence 87, Application US/11036257
; Publication No. US20060148680A1
; GENERAL INFORMATION:
; APPLICANT: KIELISZEWSKI, MARCIA
; APPLICANT: XU, JIANFENG
; APPLICANT: KOPCHICK, JOHN J.
; APPLICANT: OKADA, SHIGERU
; TITLE OF INVENTION: GLYCOPROTEINS PRODUCED IN PLANTS AND METHODS OF
; TITLE OF INVENTION: THEIR USE
; FILE REFERENCE: 27211/04081
; CURRENT APPLICATION NUMBER: US/11/036,257
; CURRENT FILING DATE: 2005-01-14
; PRIOR APPLICATION NUMBER: 60/602,562
; PRIOR FILING DATE: 2004-08-18
; PRIOR APPLICATION NUMBER: 60/582,027
; PRIOR FILING DATE: 2004-06-22
; PRIOR APPLICATION NUMBER: 60/536,486
; PRIOR FILING DATE: 2004-01-14
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 87
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: amino acid construct
US-11-036-257-87

Query Match 89.1%; Score 855.5; DB 7; Length 226;
Best Local Similarity 85.2%; Pred. No. 1.5e-75;
Matches 173; Conservative 3; Mismatches 12; Indels 15; Gaps 1;

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Qy          1 MALTFALLVALLVLSCKSSCSVG--------------CDLPQTHSLGSRRTLMLLAQMR 45
              ||  ||  : :||    :| |                |||||||||||||||||||||
Db          4 MASLFATFLVVLVSLSLASPSPSPSPSPSPSPSPSPSPCDLPQTHSLGSRRTLMLLAQMR 63

Qy         46 RISLFSCLKDRHDFGFPQEEFGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLD 105
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 RISLFSCLKDRHDFGFPQEEFGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLD 123

Qy        106 KFYTELYQQLNDLEACVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEV 165
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 KFYTELYQQLNDLEACVIQGVGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEV 183

Qy        166 VRAEIMRSFSLSTNLQESLRSKE 188
              |||||||||||||||||||||||
Db        184 VRAEIMRSFSLSTNLQESLRSKE 206
```

RESULT 12
US-11-429-276-386
; Sequence 386, Application US/11429276
; Publication No. US20060194735A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF564
; CURRENT APPLICATION NUMBER: US/11/429,276
; CURRENT FILING DATE: 2006-05-08
; PRIOR APPLICATION NUMBER: 10/775,204
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: PCT/US02/40891
; PRIOR FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: 60/341,811
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/360,000
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: 60/378,950
; PRIOR FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: 60/398,008
; PRIOR FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: 60/411,355
; PRIOR FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: 60/414,984
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: 60/417,611
; PRIOR FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: 60/420,246
; PRIOR FILING DATE: 2002-10-23
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2222
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 386
; LENGTH: 769
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-429-276-386

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  Query Match             89.1%;  Score 855.5;  DB 7;  Length 769;
  Best Local Similarity   92.9%;  Pred. No. 7e-75;
  Matches  170;  Conservative    2;  Mismatches   10;  Indels    1;  Gaps    1;

Qy          7 LLVALLVLSCKSSCSV-GCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFGFPQEE 65
              || | | |    :  :  |||||||||||||||||||||||||||||||||||||||||||
Db          2 LLQAFLFLLAGFAAKISACDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFGFPQEE 61

Qy         66 FGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEACVIQG 125
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 FGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEACVIQG 121

Qy        126 VGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNLQESLR 185
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 VGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNLQESLR 181

Qy        186 SKE 188
              |||
Db        182 SKE 184
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RESULT 13
US-11-429-276-407
; Sequence 407, Application US/11429276
; Publication No. US20060194735A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF564
; CURRENT APPLICATION NUMBER: US/11/429,276
; CURRENT FILING DATE: 2006-05-08
; PRIOR APPLICATION NUMBER: 10/775,204
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: PCT/US02/40891
; PRIOR FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: 60/341,811
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/360,000
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: 60/378,950
; PRIOR FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: 60/398,008
; PRIOR FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: 60/411,355
; PRIOR FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: 60/414,984
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: 60/417,611
; PRIOR FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: 60/420,246
; PRIOR FILING DATE: 2002-10-23
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2222
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 407
; LENGTH: 769
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-429-276-407

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  Query Match             89.1%;  Score 855.5;  DB 7;  Length 769;
  Best Local Similarity   92.9%;  Pred. No. 7e-75;
  Matches  170;  Conservative    2;  Mismatches   10;  Indels    1;  Gaps    1;

Qy          7 LLVALLVLSCKSSCSV-GCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFGFPQEE 65
              || | | |    :  :  |||||||||||||||||||||||||||||||||||||||||||
Db          2 LLQAFLFLLAGFAAKISACDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFGFPQEE 61

Qy         66 FGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEACVIQG 125
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 FGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEACVIQG 121

Qy        126 VGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNLQESLR 185
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 VGVTETPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNLQESLR 181

Qy        186 SKE 188
              |||
Db        182 SKE 184
```

RESULT 14
US-11-429-276-402
; Sequence 402, Application US/11429276
; Publication No. US20060194735A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF564
; CURRENT APPLICATION NUMBER: US/11/429,276
; CURRENT FILING DATE: 2006-05-08
; PRIOR APPLICATION NUMBER: 10/775,204
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: PCT/US02/40891
; PRIOR FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: 60/341,811
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/360,000
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: 60/378,950
; PRIOR FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: 60/398,008
; PRIOR FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: 60/411,355
; PRIOR FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: 60/414,984
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: 60/417,611
; PRIOR FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: 60/420,246
; PRIOR FILING DATE: 2002-10-23
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2222
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 402
; LENGTH: 774
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-429-276-402

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  Query Match             88.9%;  Score 853.5;  DB 7;  Length 774;
  Best Local Similarity   95.5%;  Pred. No. 1.1e-74;
  Matches  168;  Conservative    2;  Mismatches    5;  Indels    1;  Gaps    1;

Qy         14 LSCKSSCSVG-CDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFGFPQEEFGNQFQK 72
              |   |  ::| |||||||||||||||||||||||||||||||||||||||||||||||||
Db        599 LVAASQAALGLCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFGFPQEEFGNQFQK 658

Qy         73 AETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEACVIQGVGVTETP 132
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        659 AETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEACVIQGVGVTETP 718

Qy        133 LMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNLQESLRSKE 188
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        719 LMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNLQESLRSKE 774
```

RESULT 15
US-11-429-276-1300
; Sequence 1300, Application US/11429276
; Publication No. US20060194735A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF564

; CURRENT APPLICATION NUMBER: US/11/429,276
; CURRENT FILING DATE: 2006-05-08
; PRIOR APPLICATION NUMBER: 10/775,204
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: PCT/US02/40891
; PRIOR FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: 60/341,811
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/360,000
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: 60/378,950
; PRIOR FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: 60/398,008
; PRIOR FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: 60/411,355
; PRIOR FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: 60/414,984
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: 60/417,611
; PRIOR FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: 60/420,246
; PRIOR FILING DATE: 2002-10-23
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2222
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1300
; LENGTH: 774
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-429-276-1300

Query Match 88.9%; Score 853.5; DB 7; Length 774;
Best Local Similarity 95.5%; Pred. No. 1.1e-74;
Matches 168; Conservative 2; Mismatches 5; Indels 1; Gaps 1;

```
Qy          14 LSCKSSCSVG-CDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFGFPQEEFGNQFQK 72
               |    |  ::| ||||||||||||||||||||||||||||||||||||||||||||||||
Db         599 LVAASQAALGLCDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFGFPQEEFGNQFQK 658

Qy          73 AETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEACVIQGVGVTETP 132
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         659 AETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEACVIQGVGVTETP 718

Qy         133 LMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNLQESLRSKE 188
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         719 LMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNLQESLRSKE 774
```

Search completed: October 14, 2006, 08:07:25
Job time : 40 secs

STIC-Biotech/ChemLib

From: Seharaseyon, Jegatheesan
Sent: Thursday, October 12, 2006 7:56 AM
To: STIC-Biotech/ChemLib
Subject: RE: Re:10/650350

Hi,
Sorry. the serial nimber of the case was typed wrong.
It is 10/653350. Therefore, please search SEQ ID NO:1 of 10/653350.

Thanks in advance,
Seyon.

-----Original Message-----
From: STIC-Biotech/ChemLib
Sent: Wednesday, October 11, 2006 4:56 PM
To: Seharaseyon, Jegatheesan
Subject: RE: Re:10/650350

There is no valid CRF for this serial number, please provide us with another valid serial number. Thank you

LEONARD 2-2520

-----Original Message-----
From: Seharaseyon, Jegatheesan
Sent: Wednesday, October 11, 2006 4:51 PM
To: STIC-Biotech/ChemLib
Subject: Re:10/650350

Hi,
Please search SEQ ID NO: 1 of 10/650350 in th commercial databases.
Please provide paper copy of the search results.

Thanks,
SEHARASEYON
Box Rem. 4C70,
Rem 4C61
2-0892.

****
Searcher:_____
Searcher Phone:_____
Date Searcher Picked up:_____
Date completed:_____
Searcher Prep Time:_____
Online Time:_____

****
Type of Search
NA#_____ AA#:_____
S/L:_____ Oligomer:_____
Encode/Transl:_____
Structure #:_____Text:____
Inventor:_____ Litigation:___

****
Vendors and cost where applicable
STN:_____
DIALOG:_____
QUESTEL/ORBIT:_____
LEXIS/NEXIS:_____
SEQUENCE SYSTEM:_____
WWW/Internet:_____
Other (Specify):_____